

10/04/03

GenCore version 5.1.3
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OK nucleic - nucleic search, using sw model

Run on: November 30, 2002, 07:42:58 : Search time 384 Seconds
(without alignments)
16221.425 Million cell updates/sec

Database 8

Sequence: 1 atggcgtggttaaggttgcga.....gtcatcaaggggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database 8

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2768.2	99.8	2782	24 ABN83428 Human transporter
2	2768.2	98.8	2781	23 ABN83428 Human transporter
3	1784.8	64.5	126512	24 ABN83429 Human transporter
4	1326.4	48.0	2814	22 ABN83429 Human transporter
5	1277.8	46.2	4291	21 AAC75706 Human ORX ORP1261
6	1227.8	44.4	4087	24 AAD24450 Bovine NCK-1 CDNA
7	1208.8	43.7	5438	23 ABV24305 Human prostate exp
8	897.4	32.4	1187	23 AAS90968 DNA encoding novel
9	787.2	28.5	1836	22 ABA64480 Human foetal liver

10	787.2	28.5	1836	22 ABA31619
11	787.2	28.5	1836	22 AAK12937
12	787.2	28.5	1836	22 AAI19464
13	787.2	28.5	1836	22 AAI44657
14	787.2	28.5	1836	23 ABS12734
15	593.2	21.4	4546	23 ABL09809
16	363	13.1	363	22 AAI85824
17	319	11.5	24221	23 ABL09808
18	219.4	7.9	381	22 ABA42496
19	219.4	7.9	381	22 ABA52926
20	219.4	7.9	381	22 ABA22706
21	219.4	7.9	381	22 AAK01175
22	219.4	7.9	381	22 AAK26636
23	219.4	7.9	381	22 AAI11264
24	219.4	7.9	381	22 AAI32530
25	219.4	7.9	381	22 AAI01178
26	219.4	7.9	381	22 AAB01229
27	198.8	7.2	458	22 AAB98605
28	198	7.2	325	22 ABA11549
29	186.4	6.7	491	22 ABA52385
30	186.4	6.7	491	22 ABA22180
31	186.4	6.7	491	22 AAK00656
32	186.4	6.7	491	22 AAK26106
33	186.4	6.7	491	22 AAI10735
34	186.4	6.7	491	22 AAI31993
35	186.4	6.7	491	22 AAI00663
36	186.4	6.7	491	22 ABA00690
37	186.4	6.7	276	22 ABA47127
38	186.2	6.7	276	22 ABA65009
39	186.2	6.7	276	22 ABA32117
40	186.2	6.7	276	22 AAK13435
41	186.2	6.7	276	22 AAK39172
42	186.2	6.7	276	22 AAI19981
43	186.2	6.7	276	22 AAI5179
44	186.2	6.7	276	22 AAI05691
45	186.2	6.7	276	22 ABA13255

ALIGNMENTS

RESULT 1				
ID	ABN83428	standard; CDNA; 2782 BP.		
AC	ABN83428;			
DT	21-AUG-2002	(first entry)		
DE	Human transporter protein coding sequence.			
KW	Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;			
KW	spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.			
OS	Homo sapiens.			
EH	key	location/qualifiers		
FT	CDS	10..2775		
FT		/*tag= a		
FT		/product= "Human transporter"		
PN	WO200233086-A2.			
PD	25-APR-2002.			
PF	17-OCT-2001; 2001WO-US32152.			
PR	17-OCT-2000; 2000US-240836P.			
PR	13-MAR-2001; 2001US-0804474.			
PA	(PEKE) PE CORP NY.			
XX	Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;			

PI Beasley EM;
XX
XX MPI: 2002-479677/51.
DR P-PSDB: AB883246.
XX
PT Human transporter peptide related to sodium/calcium exchanger subfamily
PT for identifying modulators useful for treating a disease or condition
PT mediated by human transporter protein
XX
XX Claim 4; Fig 1; 200pp; English.
XX
CC The present sequence is the coding sequence of a human transporter
CC protein, which is related to the sodium/calcium exchanger subfamily.
CC Experimental data indicates expression of the transporter gene in humans
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR.
XX
XX Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 other;

Query Match 99.8%; Score 2761.2; DB 24; Length 2782;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCGGTGTTAAGGTTGACGCTCTACCTCTGCTTCTTCCATTTTGGGCTGTTACC 60
DB 10 ATGGCGGTGTTAAGGTTGACGCTCTACCTCTGCTTCTTCCATTTTGGGCTGTTACC 69
QY 61 TTTTGTCTCTTCTGATGATGCTTCGAGCAGAGGCTGTGGCTCAGGAGGAGCTGCCAAGC 120
DB 70 TTTTGTCTCTTCTGATGATGCTTCGAGCAGAGGCTGTGGCTCAGGAGGAGCTGCCAAGC 129
QY 121 ACAGGCGAAGCAATGAGTCTCTTCAAGGCTCATCGGACTGCAAGAGAGGCTGTCATCTG 180
DB 130 ACAGGCGAAGCAATGAGTCTCTTCAAGGCTCATCGGACTGCAAGAGAGGCTGTCATCTG 189
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DB 190 CCATCTGATACCCGAGAGACCTTCCCTTGGGAGCAAGATGGCAGAGGCTATGTCTAT 249
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DB 250 TTTTGTGCGCTGATATACATGTTCTTGGGGTGCATCATTTGGCTGACCGCTTCATGCA 309
QY 301 TCTATTGAGTCATCACCCTCTCAAGAGAGGAGTGCAATTAAAGAAACCAATGAGAA 360
DB 310 TCTATTGAGTCATCACCCTCTCAAGAGAGGAGTGCAATTAAAGAAACCAATGAGAA 369
QY 361 ACAGGCAACCACTATTCCGGTCTGGAATGAACCTGTCACCACTGACCTTATGGCC 420
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QY 421 CTGGGTTCTCTGCTCTGAGATACCTCTCTTAAATTAGGTTGGTCATGGGTTTC 480
DB 430 CTGGGTTCTCTGCTCTGAGATACCTCTCTTAAATTAGGTTGGTCATGGGTTTC 489
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DB 550 ATCATTTGGCATCTGTCTACGTGATCCAGAGCGGAGAGACTGCAAGATCAAGCATCTA 609
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DB 610 CGAGTCTCTTCATCAACCGTCTGAGATATCTTCCCTACATCTGGCTCTATATGAT 669
QY 661 CTGGCAGTCTTCTCCCTGCTGTGTGTCAGAGTTGGAGAGGCTCTCAGCTCTTCTTC 720
DB 670 CTGGCAGTCTTCTCCCTGCTGTGTGTCAGAGTTGGAGAGGCTCTCAGCTCTTCTTC 729
QY 721 TTTTCCAGTGTGTCTCTTCTGGGCTGGGTGGAGATTAACGACTGCTTCTCAAAATAC 780
DB 730 TTTTCCAGTGTGTCTCTTCTGGGCTGGGTGGAGATTAACGACTGCTTCTCAAAATAC 789
QY 781 ATGCACAAAAAGTACCGCAGACAAACACCGAGGAATTAATAGACAGAGGGTGAC 840
DB 790 ATGCACAAAAAGTACCGCAGACAAACACCGAGGAATTAATAGACAGAGGGTGAC 849
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DB 850 CACCTTAAGGCGATTTGATGATGGGAAAAATGATGAATTTCCATTTTCTAGATGGGAC 909
QY 901 CTGGTGGCCCTGGAAGGGAAGTGGATGATGCCCGCAGAGAGATGCCGATCTTC 960
DB 910 CTGGTGGCCCTGGAAGGGAAGTGGATGATGCCCGCAGAGAGATGCCGATCTTC 969
QY 961 AAGATCTGAAGCAAAAAACCCAGAGAGACTTAGATAGCTGTGGATGGCCAA 1020
DB 970 AAGATCTGAAGCAAAAAACCCAGAGAGACTTAGATAGCTGTGGATGGCCAA 1029
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DB 1030 TACTATGCTCTTCCACCAAGAGAGAGCGCGCTTCTACCGTATCCAGCCACTCGT 1089
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QY 1681 ACAGTATGCTGCCCTTTAGACAGTAGAAGGAGCCAAAGGTTGGCGTGAAGCTTT 1740
DB 1690 ACAGTATGCTGCCCTTTAGACAGTAGAAGGAGCCAAAGGTTGGCGTGAAGCTTT 1749
QY 1741 GAAGACACATATGAGGAGTGTGAATTCAGAGATGATGAATCTGAAAAACATAGAGGTT 1800
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DB 1810 AAAATAGTATGATGAGAGAGATACGAAGGCAAGAGATTTCTTCAATGTGCTGTGAA 1869

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QY 1861 CCGAATGGATGAGACGTGATATCATGATGACAGACAGAGAGTGCATATGGAAGA 1920
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QY 1921 GAGGAGGCCAAGAGATAGACAGATGGAAGCCAGTATTTGGTGAACACCCCAACAA 1980
DB 1930 GAGGAGGCCAAGAGATAGACAGATGGAAGCCAGTATTTGGTGAACACCCCAACAA 1989
QY 1981 GAAGTCATCATTTGAAGAGTCTATGATGTTCAAGACTACGGTGACAACTGATCAAGA 2040
DB 1990 GAAGTCATCATTTGAAGAGTCTATGATGTTCAAGACTACGGTGACAACTGATCAAGA 2049
QY 2041 ACAAACCTGGGCTTGGTGGGAGCCATTCCTGGAGGAGACAGTCAATGAGAGCCATC 2100
DB 2050 ACAAACCTGGGCTTGGTGGGAGCCATTCCTGGAGGAGACAGTCAATGAGAGCCATC 2109
QY 2101 ACCGTCAGTGCAGCAGGAGGATGAGATGATGAATCCGGGAGAGAGAGGCTGCCCTCC 2160
DB 2110 ACCGTCAGTGCAGCAGGAGGATGAGATGATGAATCCGGGAGAGAGAGGCTGCCCTCC 2169
QY 2161 TGCCTTGACTACGTACATGACATCTCTGACTGCTCTTGAGAGGTGCTGTTGCTGTG 2220
DB 2170 TGCCTTGACTACGTACATGACATCTCTGACTGCTCTTGAGAGGTGCTGTTGCTGTG 2229
QY 2221 CCCCCACAGAGTACGTCGACGAGGCTGGGCTGCTGCGGCTGCTCCATTCCTCATATG 2280
DB 2230 CCCCCACAGAGTACGTCGACGAGGCTGGGCTGCTGCGGCTGCTCCATTCCTCATATG 2289
QY 2281 ATGCTCACCCGATCATATTGGGAGACCTGCGCTGCACTTGGCTGACATTTGGTCTCAA 2340
DB 2290 ATGCTCACCCGATCATATTGGGAGACCTGCGCTGCACTTGGCTGACATTTGGTCTCAA 2349
QY 2341 GATTAGTACACAGCTGTTGTTTTCGTGGCATTTGGCACTCTGTGCCAGATACGTTGCC 2400
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QY 2401 ACAAAGGCTGCGCTGAGAGATGATATGACAGAGGCTGCACTTGGCAAGGATGAGAGG 2460
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DB 2710 AGCTGTGGCTCTCTACATCTCTTTGGCACACTTGAAGGCTATTGCTACATCAAGGG 2769
QY 2761 TTCTTA 2766
DB 2770 TTCTTA 2775

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RESULT 2
AB04756
ID AB04756 standard; cDNA; 2781 BP.
AC AB04756;
XX
DT 25-FEB-2002 (first entry)

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XX DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.
XX KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
XX KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
XX KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiac; Vaccine;
XX KW coronary heart disease; renal failure; ischemic disorder;
XX KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.
XX OS Homo sapiens.
XX FH Key
XX FH CDS
XX FT Location/Qualifiers
XX FT 1..2781
XX FT /*tag= a
XX FT /partial
XX FT /product= "Human natrium(+)-calcium(2+) exchanger form 3
XX FT protein, HNCX3"
XX FT /note= "No stop codon given"
XX PN MO200183744-A2.
XX PD 08-NOV-2001.
XX PF 30-APR-2001; 2001WO-EP04886.
XX PR 02-MAY-2000; 2000EP-0109080.
XX PA (MERCK) MERCK PATENT GMBH.
XX PI Wilm C;
XX DR MPI: 2002-041493/05.
XX DR P-PDB: AAM47745.
XX PT New polypeptide, useful as vaccines for inducing immune response
XX PT against diseases such as myocardial infarction, arrhythmia, ischemic
XX PT disorders, renal disorders in mammal.
XX PS Claim 4; Page 34-38; 41pp; English.
XX CC The present sequence is the coding sequence for human Natrium(+)-Calcium
XX CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
XX CC 14. HNCX3 and its coding sequence are useful for treating acute and
XX CC chronic cardiac failure of different aetiologies, myocardial infarction,
XX CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
XX CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
XX CC acute and chronic renal failure, ischemic disorders of skeletal muscle
XX CC and ischaemic brain disorders of different aetiologies.
XX SQ Sequence 2781 BP; 658 A; 678 C; 765 G; 680 T; 0 other;

Query Match 98.8%; Score 2733.4; DB 24; Length 2781;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2762; Conservative 0; Mismatches 1; Indels 18; Gaps 1;

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DB 1 ATGGCGGTGATTAAGTTGAGGCTCTACCTGCTTCCATTTTGGGCTGTACC 60
QY 61 TTTGTGCTCTTCTGTAATGTTTCGAGCAGAGGCTGTGGCTCAGAGGAGCTGCACAGC 120
DB 61 TTTGTGCTCTTCTGTAATGTTTCGAGCAGAGGCTGTGGCTCAGAGGAGCTGCACAGC 120
QY 121 ACAGGCGACAAACAGATAGTCTGTTGAGGTCATCGGACTGCAAGAGAGGCTGTCATCTG 180
DB 121 ACAGGCGACAAACAGATAGTCTGTTGAGGTCATCGGACTGCAAGAGAGGCTGTCATCTG 180
QY 181 CCAATCTGTACCCGAGAACCTTCCCTTGGGAGCAAGATTGGCCAGGGTCATGCTAT 240
DB 181 CCAATCTGTACCCGAGAACCTTCCCTTGGGAGCAAGATTGGCCAGGGTCATGCTAT 240
QY 241 TTTGTGCGCTGATATACATGTTCTTGGGAGTCCATGCTGACCGCTTCATGGCA 300
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Db 241 TTGTGGCCCTGATATACATGTTCCCTGGGGTGTCCATCATGTCGACCGCTTCATGCA 300
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Db 301 TCTATGAAGTCATCACCCTCAAGAGAGGGAGGACAAATTAAGAAACCAAGAGAA 360
QY 361 ACAGACACACACACTATTCGGGTCTGGAATGAACCTGTCTCAACCTGACCCCTATGACC 420
Db 361 ACAGACACACACACTATTCGGGTCTGGAATGAACCTGTCTCAACCTGACCCCTATGACC 420
QY 421 CTGGGTTCTCTGCTCCGAGATACCTCTCTTTAATTGAGGTGTGTGTCATGGCTTC 480
Db 421 CTGGGTTCTCTGCTCCGAGATACCTCTCTTTAATTGAGGTGTGTGTCATGGCTTC 480
QY 481 ATTGCTGTGATCTGGGACCTTCTACATTTGTAGGAGCTGCAAGCTTAAACATGTTCTC 540
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Db 721 TTTTCAGTGTGTCTCTCTGCTGCTGGCTGGAGATAAACAGCTCTCTCTCTCTCTCTAC 780
QY 781 ATGCACAAAAAGTACCCGACAGACAAACACCGAGGAATTATCATAGAGACAGAGGTGAC 840
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QY 1381 CAGAAGAGTTCTCCGTGGGCATATTTGATGACGACATTTTGTAGAGAGATGAACACTTC 1440
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QY 1801 AAAATAGTATGAGAGGAATACGAAAGCAGAGAAATTTCTTATTTGCCCTTGTTGAA 1860
Db 1801 AAAATAGTATGAGAGGAATACGAAAGCAGAGAAATTTCTTATTTGCCCTTGTTGAA 1860
QY 1861 CCGAAATGATGAGAACTGGAAATTC-----AGATGTGACAGACAG 1920
Db 1861 CCGAAATGATGAGAACTGGAAATTC-----AGATGTGACAGACAG 1920
QY 1903 AAGCTGACTATGAGAAAGAGAGAGCCCAAGAGATACAGAGATGGGAAAGCCAGTATTTG 1962
Db 1903 AAGCTGACTATGAGAAAGAGAGAGCCCAAGAGATACAGAGATGGGAAAGCCAGTATTTG 1962
QY 1921 AAGCTGACTATGAGAAAGAGAGAGCCCAAGAGATACAGAGATGGGAAAGCCAGTATTTG 1980
Db 1921 AAGCTGACTATGAGAAAGAGAGAGCCCAAGAGATACAGAGATGGGAAAGCCAGTATTTG 1980
QY 1963 GGTGAGACCCCAAACTAGAAAGTATCATATGAAAGTCTATGAGTTCAAGACTTACGGTG 2022
Db 1963 GGTGAGACCCCAAACTAGAAAGTATCATATGAAAGTCTATGAGTTCAAGACTTACGGTG 2022
QY 2023 GACAACTGATCAAGAGACAAACCTGCGCTTGTGTTGGGAGCCCATTCCTGAGAGGAC 2082
Db 2023 GACAACTGATCAAGAGACAAACCTGCGCTTGTGTTGGGAGCCCATTCCTGAGAGGAC 2082
QY 2083 CAGTTCAATGAGAGCCATCACCGCTGACAGTCAAGAGAGGATGAGATGATGATCCGGG 2142
Db 2083 CAGTTCAATGAGAGCCATCACCGCTGACAGTCAAGAGAGGATGAGATGATGATCCGGG 2142
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Db 2101 CAGTTCAATGAGAGCCATCACCGCTGACAGTCAAGAGAGGATGAGATGATGATCCGGG 2160
QY 2143 GAGGAGAGGCTGCCCTCTGCTTGTGACTATGCTACATCTCTGACTGTCTTCTGGAAG 2202
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QY 2221 GTGCTGTTGCTGTGTGCCCCCAGAGATGACAGGCTGAGGCTGCTGCTGCGCGTC 2280
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Db 2761 TATTGCTACATCAAGGGGTTTC 2781

RESULT 3
ABN83429
ID ABN83429 standard; DNA; 126512 BP.
XX
AC ABN83429;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human transporter protein gene.
XX
KM Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KM spleen; testis; leukocyte; foetal brain; chromosome 14; gene;
KW single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key
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Query Match 64.5%: Score 1784.8: DB 24: Length 126512:
Best Local Similarity 99.9%: Pred. No. 0:
Matches 1786: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

QY 1 ATGGCGTGGTTAAAGTTGACGCTCTCACCCTCTCCCTCCATTTTGGGCTGTACC 60
FT ATGGCGTGGTTAAAGTTGACGCTCTCACCCTCTCCCTCCATTTTGGGCTGTACC 60
DB 2010 ATGGCGTGGTTAAAGTTGACGCTCTCACCCTCTCCCTCCATTTTGGGCTGTACC 2069
FT ATGGCGTGGTTAAAGTTGACGCTCTCACCCTCTCCCTCCATTTTGGGCTGTACC 2069
QY 61 TTGTGCTCTTCCGTAATGCTCTTCGAGCAGAGCTGGTGGCTCAGGGGACGTCCAAAC 120
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DB 2070 TTGTGCTCTTCCGTAATGCTCTTCGAGCAGAGCTGGTGGCTCAGGGGACGTCCAAAC 2129
FT TTGTGCTCTTCCGTAATGCTCTTCGAGCAGAGCTGGTGGCTCAGGGGACGTCCAAAC 2129
QY 121 ACAGGGCAGAACATGAGTCTCTGTTACGGGTCATCGGACCTCAGAGGGGTGATCCTG 180
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QY 841 CACCTTAAGGCGATTTGATGATGATGGGAAATGATGATCCCTTTTCTAGATGGGAC 900
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Dp	2970	AAGGATCTGAAGCAAAAACACCAGAAAGGACTTATGATACAGCTGTGAGATGGCCAT	3029
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Dp	3030	TACTATGCTTTTCCCAACCAAGAAAGACCGCGCTTCTACCGTATCCAAAGCCACTG	3089
Qy	1081	ATGATGACTGTGTGACGACATATCTGAGAAACATGCGAGCAAGAACCCAAAGAGCC	1140
Dp	3090	ATGATGACTGTGTGACGACATATCTGAGAAACATGCGAGCAAGAACCCAAAGAGCC	3149
Qy	1141	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTATTTTCCAAAGTCTT	1200
Dp	3150	TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTATTTTCCAAAGTCTT	3209
Qy	1201	GACCATGTTCTTACACAGTCCGCGGAGACTGTGGGGCTGTCTCTACAGTGTGAG	1260
Dp	3210	GACCATGTTCTTACACAGTCCGCGGAGACTGTGGGGCTGTCTCTACAGTGTGAG	3269
Qy	1261	AAAGGGGGAACATGTCAAAGACCAATGATGTGTGACTACAAAACAGAGATGTTCTGC	1320
Dp	3270	AAAGGGGGAACATGTCAAAGACCAATGATGTGTGACTACAAAACAGAGATGTTCTGC	3329
Qy	1321	AATGCGAGGGCTACATATGACTTACACAGAGGCGAGGTGTCTGAAGCCAGAGAGACC	1380
Dp	3330	AATGCGAGGGCTACATATGACTTACACAGAGGCGAGGTGTCTGAAGCCAGAGAGACC	3389
Qy	1381	CAGAAAGAGTTCCTCGGGGCAATTTGATGACGACATTTTGAAGAGATGAACACTTC	1440
Dp	3390	CAGAAAGAGTTCCTCGGGGCAATTTGATGACGACATTTTGAAGAGATGAACACTTC	3449
Qy	1441	TTTGTAGTTGAGCAATGTCCGCATAGAGAGAGACCCAGAGAGGGGATGCCCTCA	1500
Dp	3450	TTTGTAGTTGAGCAATGTCCGCATAGAGAGAGAGACCCAGAGAGGGGATGCCCTCA	3509
Qy	1501	GCAATATTCAACAGTCTCCCTTGCTCGGGGCGTGCCTGACCTCCCTGTGTGGCCACA	1560
Dp	3510	GCAATATTCAACAGTCTCCCTTGCTCGGGGCGTGCCTGACCTCCCTGTGTGGCCACA	3569
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Dp	3570	GTTACCATCTTGGATGATGACCAATGCAGGACATCTTCACTTTGAATGTGATACTATTCAT	3629
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Dp	3630	GTCAGTAGAGTATGTGTATTATGAGAGTCAAGTCTCGGACATCAAGTCCCGGGGT	3689
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Dp	3690	ACAATCATGCTCCCTTTAGAGACAGTAAAGGAGACAGCCAAAGGTGGCGGTGAGACTTT	3749
Qy	1741	GAAAGACCATATGGGAGGTTGGAATTCAGGAATGATGAACACTGTGAAA 1788	
Dp	3750	GAAAGACCATATGGGAGGTTGGAATTCAGGAATGATGAACACTGTGTGAA 3797	

RESULT 4	
AAH57377	
ID	AAH57377 standard; cDNA: 2814 BP.
XX	
AC	
XX	AAH57377:
DT	10-SEP-2001 (first entry)
XX	
DE	Human heart cell specific cDNA sequence SEQ ID NO:217.
XX	
KW	Human; tissue specific; diagnosis; brain; heart; skeletal muscle;
lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas;	

KW	metabolic disease; developmental disease; cyrostatic; immunomodulatory;
XV	neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX	Homo sapiens.
OS	WO200132927-A2.
PN	10-MAY-2001.
PD	02-NOV-2000; 2000MO-US0396.
XX	04-NOV-1999; 99US-0163508.
PF	(INCY-) INCYTE GENOMICS INC.
PA	Sornasse T, Sellhammer JJ, Watson GA;
XX	WPJ: 2001-291057/30.
DR	New cell and tissue specific polynucleotides useful for diagnosis,
PT	prognosis or monitoring of treatments for disorders where the gene is
PT	associated with a cancer, immunopathology or neuropathology -
XX	Claim 1; Page 146-147; 327pp; English.
PS	AAM57161 to AAM57576 represent cell and tissue specific polynucleotide
CC	sequences (I). (I) can have cytostatic, immunomodulatory and
CC	neuroprotective activities, and can be used in gene therapy. (I) and
CC	proteins (II) encoded by them are used in high throughput screening
CC	assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC	limerics, peptides, proteins, agonists, antagonists, antibodies or
CC	their fragments, immunoglobulins, inhibitors, drug compounds and
CC	pharmaceutical agents. Expression of (I) in a sample indicates the
CC	differentiation of embryonic stem cells into a tissue selected from
CC	brain, heart, kidney, liver, lung, skeletal muscle or pancreatic
CC	tissues. (I) and (II) are used to produce an expression profile that
CC	defines a metabolic or developmental process, treatment, condition,
CC	disease or disorder. The gene profile can be used for diagnosis,
CC	prognosis or monitoring of treatments and for investigating a
CC	predisposition to a disorder where the gene is associated with a
CC	cancer, immunopathology or neuropathology.
XX	
SQ	Sequence 2814 BP; 754 A; 579 C; 718 G; 763 T; 0 other;
	Query Match 48.0%; Score 1326.4; DB 22; Length 2814;
	Best Local Similarity 69.8%; Pred. No. 0;
	Matches 1893; Conservative 0; Mismatches 756; Indels 63; Gaps 5;
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Dd	
	112 GAATGAAGGAAGGAAGAAATGAAATGAGTAGTGATGACTGATCATATTACTGTAAGAAA 171
OY	169 GGTGATACCTCGCCAATCTGATACCCGGAGAACCTTCCCTGGGGCAAGATTGCCAGG 228
Dd	
	172 GGGGGATTGTCGCCATTTGGGAACCCCAAGACCCTTTTGGGGCAAAAAATTGGCTAGA 221
OY	229 GTCATGTCTAATTTTGGGCCCTGATATTAATCTTCCCTGGGGGTCATCATTTGGTAC 288
Dd	
	232 GCTACTGTGTATTTTGTGBCCATGSGTCTACTATGTTTTCTTGAGTCTCTATCATAGCTGAT 291
OY	289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGAGAGAGTGCATAATTAGAAA 348
Dd	
	292 CGGTTTCATGTCCTCTATATGAGATCATACATCTCAAGAAAAAAATTAACCATTAAGAAA 351
OY	349 CCCAATGGAAGAACAGCACAACACATATTGGGTCTGGAAATGAAATGTCCTCCAACTG 408
Dd	
	352 CCCAATGGAAGAACACACCAAGACAACGTGAGATCTGGAATGAAACAGTTTCTAAACTG 411
OY	409 ACCCTAATGGGCGGGGGTCTCTGTCNCNAGATTAATCCCTTTAATTAAGAGTGTGT 468
Dd	
	412 ACCTTGATGCCCCTGGGATCTTCTGCTCTCTGAGATTTCTCCTTTTCAGTAATGAAGTGTGT 471
OY	469 GGTCATGGGTTTCATTTGCTGTGATCTGGGACCTTCTACCAATTGTAGGAGATGACGCTTC 528

Db 472 GGCATTAACCTCAGCGAGGAGACCTGCTCTAGCACCAATCGTGGGAAGTGTGATTC 531
OY 529 AACATGTTTCATCATATTTGGATCTGTGTACGTACGTATCCAGACGGAGAACACGCGAAG 588
Db 532 AATATGTTTCATCATATTTGGATCTGTGTACGTATCCAGACGGAGAACACGCGAAG 591
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Db 592 ATTAAGCATTTGGGTGCTCTTTGTGACAGACCCCTGGACATCTTTGCCATACACCTCG 651
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Db 652 CTTCATATTAATTTGT 711
OY 709 ACT 768
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OY 880 TCCCATTTTCTAGATGGGAACCTGTGGCCCTGGAGGAGGAG----- 921
Db 892 TCTCATGTGTGAAATTTCTTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 951
OY 922 GAACTGATGAGTCCCGACAGAGATGATCGGATTTCTCAAGGATCTGAAACAAAACAC 981
Db 952 GATGATGAAAGGATGAGCGGAAATGAGCTAGATTCGAAAGAACTTAAACAGAAAGCAT 1011
OY 982 CCAAGAGAAGCTTATGATCAGCTGTGTGAGATGTGCCAATTAATGCTCTTTCCACCAA 1041
Db 1012 CCAATATAAAGAAATGAGCAATTAATAGAAATTAATTAATTAATTAATTAATTAATTA 1071
OY 1042 CAGAAAGACCGGCTCTTCTACCGTATCCAGACCACTGATGATGAGCTGTGTGAGCAAT 1101
Db 1072 CAAAAGATGAGCATTTTATTCGATTCAGACTCTGCTGCTGATGATGAGCTGTGTGAG 1131
OY 1102 ATCTGAAAGAAATGAGCAGACGAAACCAAGCAAGAGGCTTCAGATGAGGAGGTGCAC 1161
Db 1132 ATTTTAAAGAGCATGACGATGACCAAGCAAGAGGCTGTGACATGACAGAGTCAAC 1191
OY 1162 ACCGATGAGCTG---AGGATTTATTTCCAGGCTCTTCTTTGACCCATGTTCTTACCAG 1218
Db 1192 ACTGAAGTGAATAATGACCCCTGTGTAGTAAATCTTCTTTGAAACAAAGGACATATCAG 1251
OY 1219 TGCCTGAGAACTGTGGGGCTGTACTCTGACAGTGGGAGGAAAGGGGAGACATGCA 1278
Db 1252 TGTCTGGAGAACTGTGTACTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1311
OY 1279 AAGACATGTAATGTGACTACAAAACAGAGAGATGTTCTGTCCAAATGCAAGGGCTGACTAT 1338
Db 1312 AACACTGTGTGTGTGACTCAGAAACAGAGATGGCACAGCAAAATGCGGGTGTGATTAT 1371
OY 1339 GAGTTTACAGAGGCGAGGTGTCTGAGCCAGAGAGACCCAGAAAGGATTTCCGTG 1398
Db 1372 GAAATTTACTGAAAGACGTGTGTGTTAAAGCTGTGTATACCCAGAAAGAAATCAGAGTG 1431
OY 1399 GGCATTAATTTGATGACATTTTGTGAGAGAGATGACACTCTTTGTAAGTTGAGCAAT 1458
Db 1432 GGTATTCATATGATGATATCTTTTGTGAGAGATGAAATTTCTTGTGTGATCTGACAT 1491
OY 1459 GTCCGATATAGAGAGAGACGACAGAGAGAGGATGCTCCAGCAATATTCACAGCTCT 1518
Db 1492 GTCAAGATATCTTGTGAAGCTTCAAGAGATGAGCATACTGGAAGC-----CAATCAT 1542
OY 1519 CCTTGGCTGTGGCTGTCTAGCCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1578
Db 1543 GTTCTACACTTGGCTGTGGCTGTCTCCCTCAGCTGTCCACACTGTATATTTTGTATGAT 1602
OY 1579 GACCATGAGGACATCTTACATTTTGAATGTGATATCTATTCATGTGAGAGATTTGAT 1638
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Db 1783 CTCGAATTCAGATGATGAAATTTGTGAAATCTTACATTTAGAAATTTGACCGGTAG 1842
OY 1819 GAATACGAAAGGCAAGAAATTTCTTCAATGCTCTGTGTGAAACCGAAATGGATGAAAGT 1878
Db 1843 GAATATGAGAAAGATGACAGTTTCTCCCTGTGTGTGAGAACCAAAATGATTAAGAA 1902
OY 1879 GGAATATCAG-----ATGTGACAGACAGAAAGCTGACTATG 1914
Db 1903 GGAATGAAAGGTGCTTACAAATACAGACGAAATATGATGACAAAGCCTGACAGC 1962
OY 1915 GAAAGAGAGAGGCGCAAGAGATGACAGAGATGGAAGACCACTGATTTGGGTGAACCCC 1974
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OY 1975 AAATGAGATCATATTTGAAGAGTCCATGATGATTTCAAGACTACGTTGACAAATCTATC 2034
Db 2023 AAGTTGGAAGGATCATTTGAAGAAATCCTATGAAATTTCAAGAGTACTGTGTGACAACTAT 2082
OY 2035 AAGAGCAAAACCTGTGGCTGTGTGTGGGACCCATCTCTGTGAGAGGACCAATTTGAG 2094
Db 2083 AAGAGCAAAACCTGTGGCTGTGTGTGGGACCTGACCTGAGAGCAAGCAAGCTTATTTGAA 2142
OY 2095 GGCATACACCGTCACTGACAGCAGGAGGATGAGATGAGATGAAATCCGGGAGAGAGGCTG 2154
Db 2143 GCTATACGTGACATGCTGTGGGAAAGATGATGACAGCATGAAATGGGGAAGAAACCTG 2202
OY 2155 CCTCTGCTTTTGAATGCTACACTCTCTGACTCTCTTGTGGAAGTGTGTGTGCTTGGCC 2214
Db 2203 CCTCTGCTTTTGAATGCTACACTCTCTGACTCTCTTGTGGAAGTGTGTGTGCTTGGCC 2262
OY 2215 TGTGTGCCCCCAGAGATGCTGCAAGGCTGTGGGCGCTGTGGCGCTGTCCATCTCATC 2274
Db 2263 TTTGCTCCCCCTACTGATATGGAATGTGGGCGGTGTTCATTTGCTCCATCTCATG 2322
OY 2275 ATTGGCATGCTCACCGCATCATGTTGGGACCTGTGCGACTTGGCTGACCATTTGGT 2334
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Db 2383 CTGAAGATTCATGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2442
OY 2395 TTTTGCAGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2454
Db 2443 TTTTGCAGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2502
OY 2455 ACGGGAGCAAGGCGCTCAATGTTCTCTGTGGGCTGTGCGGCTGTGCTGTGCTGTGCTGTG 2514
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OY 2515 ATCTACTGGCTGTGACGAGGACAGAGTTCACAGTGTGCGGCGGACACAGTGTGCTTTC 2574
Db 2563 ATCTACACGAGGACATGAGGAGAACTTCAAGATGTGCCCTGTGACACACTAGCTTCTCT 2622
OY 2575 GTCAACCTCTTTCACCATTTTGTGATTTGTGTGATCAGCTGTGCTGTGTGATCAGAGCG 2634
Db 2623 GTCACTCTCTTTCACCATTTTGTGATTTGTGTGATTTGTGTGATTTGTGTGATTTGTGTG 2682

QY 2635 CCGCACCTGGAGGAGCTGTGGCCCCGTTGGCTGCAGCTGCACACATGCGTC 2694
 DB 2683 CCAGAAATCGAGGTGAGCTGGGTGGCCCCGAGCTCCCTCATCTGCTCC 2742
 QY 2695 TTGTGAGCCTGTGCTCTCTACATCTTGTGACACTAGAGCCCTATTGCTCATC 2754
 DB 2743 TTGTGCTCTCTATGGCTCTGTACATTTCTTCTCTCTCCCTGGAGCCCTACGCGCACATA 2802
 QY 2755 AAGGGCTTTAA 2766
 DB 2803 AAGGCTTCTAA 2814
 RESULT 5
 AAC75706
 ID AAC75706 standard; cDNA; 4291 BP.
 AC AAC75706;
 XX
 DT 08-FEB-2001 (first entry)
 DE Human ORFX ORF1261 polynucleotide sequence SEQ ID NO:2521.
 XX
 KW Human: open reading frame; ORFX: detection; cytosstatic; hepatotropic;
 KW vulnerability; antiparotatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antirheumatic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antihypertensive;
 KW antiviral; antibacterial; antifungal; antineumatic; antihypertensive;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cholesterel ester storage; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW severe combined immunodeficiency; systemic lupus erythematosus; infection;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI: 2000-602362/57.
 DR P-ESDB: AAB41497.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5; Page 1807-1809; 5507pp; English.
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytosstatic; hepatotropic; vulnerability;
 CC antiparotatic; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antirheumatic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antineumatic;

CC antihypertensive; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 4291 BP; 745 A; 1405 C; 1301 G; 840 T; 0 other;
 Query Match 46.2%; Score 1277; DB 21; Length 4291;
 Best Local Similarity 69.1%; Pred. No. 0;
 Matches 1843; Conservative 0; Mismatches 775; Indels 51; Gaps 5;
 QY 130 AACATGAGTCTCTGTCAGGCTCATGACGACGACGAGGAGGCTCATCTGCAATCTGG 189
 DB 208 AGCACAAGGGGGGCGCCAGGGGCTCTACCCGCTGCACCCGGGGGTGCTGCGCCGTGG 267
 QY 190 TACCCGAGACACCTTCCCTTGGGAGACAGATTGCGAGGGTCAATGCTATTTTGGGCC 249
 DB 268 GAGCCGAGACACCCGCTGCTGGGTGACAAAGCGCGCAGGGCACTGCTATTTGGGCC 327
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 DB 328 AGGCTCATATGTTCTTGGAGAGTCCATCATCGCCGACCGCTTCAATGCGCGCATCGAG 387
 QY 310 GTCATACCTCTCAAGAGAGGAGGTGACATTTAAGAAACCAATGAGAAACACACAA 369
 DB 388 GTCATACCTCAAAAGAGAGATCACCATCACCAAGCCCAACGCTAGACACCGTG 447
 QY 370 AACACTATTCGGGTGAGATGAACTGTCTCAACCTGATCTTATGCGCCGTGGCTTC 429
 DB 448 GGCACCGTTGCGATCTGAGATGAGCGGTGTCCACCTCAAGCTCATGGCCCTGGGCTCC 507
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 QY 490 GATCTGGACCTTCTACATTTGAGGAGTGCAGCTTCAACATGTTCAATCATATGGC 549
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 QY 670 TTCTCCCTGCTGTGCTCCAGGTTTGGGAGAGGCTCTCACTCTCTTCTTCCAGTG 729
 DB 748 TTTTCCCGGCTGTGCTCCAGGTTTGGGAGGCGCTCTACCTGCTGTCTTCCGCGTG 807
 QY 730 TGTGCTCTTGGCGTGGGGGAGATTAACGATGCTCTTACAAATATGACAA 789
 DB 808 TGGCTGTATTGCTGTGATGCGCGCAGCGGCTCTTCTTACAAATGATGATCAAG 867
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 DB 868 CGGTACCGACAGCAGCAGGAGGAGCATATGAGGCGGAGGCGGAGCCCGGAAG 927
 QY 850 GGCATTGAGATGATGAGAAATGATGAATTTCCATTTTCTAGATGGAA-----889
 DB 928 AGCATGAGACGTACGCGCAGCTTCTGTTGCGGAGCGCCAGTGTAGTGTGGCGGCTG 987
 QY 900 --CCTGCTGCCCTGGAAGGAAGAGATGATGATCCCGGAGATGATGATCGGATT 957

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Qy	1078	CGTATGATGACTGGTGGCAGGCAATATCTCTAAMAAACATGACAGCAAGCAACCCAAAG	1137
Db	1168	CGGGGATGACCGGGCGCGGGAAAGCTGCTGCGAGACACGGCGGACGCCCTCGGGCAGG	1227
Qy	1138	GCCTTCACGATGACGAGGTGCAACCCAGTAGCCTTGAGAGACTTTATTTCCAAAGTCTTC	1197
Db	1228	GGGGC---GGCGGGCGAGGGCGGGGGGAGAGAGCAAGACGCGGCCACGGCCGATCTTC	1284
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Db	1285	TTTCAGGCTTACCTCTTACCACTGCTGTGGAACCTGGGGCTCGGTGCTGTGTCTCTCAGC	1344
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Db	1345	TGCCAGGGCGGGCGAGGGCAACAGCACCCTTCTACGTGATACCGCACTGAGAGCGGCTCT	1404
Qy	1318	GCCAAATGCAGGGGCTGACTATGAGTTTCACAGAGGCAACGGTGGTTCTGAAGCCAGAGAG	1377
Db	1405	GCCAAAGGGGGCTCCGACTACGAGTACAGGAGGAGGACGCTGGTTTCAACCAAGGGAG	1464
Qy	1378	ACCCAGAGAGATCTCCGCTGGGCACTAATTTGATGACAGCAATTTTTSAGAGATACAC	1437
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Qy	1438	TTCTTTGTAAGGTTGAGCAATGTCCGATGTAGAGAGAGACGACGAGAGAGGGATGGCT	1497
Db	1525	TTCTTTGCGGGGCTGTGAACTGTCCGCTGTGGGAGCGCCGAGCGCATGTTGAGCGC---	1581
Qy	1498	CCAGCAATATTCAACAGCTCTTCCCTTGCCCTGGGGCTGTCTTACGCTCCCTTGTGTGGCC	1557
Db	1582	-----GACGGCGGGGGGGGGCCCAAGGGCGGGCTGGTGGCGCGCTGCTGGGCC	1629
Qy	1558	ACAGTTACACTCTTGGATGATGACCATGCAAGCATCTTCACTTTGATGTGATCTATTT	1617
Db	1630	ACCGTCAACCTTCGGAGCGACGACACACGCGAGGCACTTCTCTTCAGAGACCGCCTGCTG	1689
Qy	1618	CATGTCAAGTAGATTAATTTGGTGTATGAGAGGTCMAAGTCTGCGGCAACATCAAGTCCCGG	1677
Db	1650	CACGTGAGCGAGTGCATGTGGCCACCGTGTGACGTGTGCTGTGCGCACTCGGGCGCGGC	1749
Qy	1678	GGTACAGTCATCGTCCCTTTAGAGACGTAGAAAGGAGCAACGCAAGGCTGGCTGAGAGC	1737
Db	1750	GGCACCGGGCCCTTCCCTACCGACGTTGGAGCGGACGCGCGGGCGGGGGCGGCTGCAC	1809
Qy	1738	TTTGAAGACACATTTGGGGAGTTGGATTCAGAGATGATGAACATGTGAACCACTAAGG	1797
Db	1810	TACAGAGGACGGCTCGGAGAGCTGTGAGTTTGGCGAGCAAGAACCATGTAACCTCTTCAG	1869
Qy	1798	GTTAAAAATAGTATGAGTGAAGAGAAATCGAAAGGCAAGCAATTTCTCATTTGCCCTTGGT	1857
Db	1870	GTGAAGATAGTTGATGACGAGAAATTCAGAAAAAGATTAATTTCTTATTTGAGCTGGGC	1929
Qy	1858	GAACCGAAATGGATGGAACCTGGAAATATAGATGTGACA-----GAC	1839
Db	1930	CAGGCCCAAGTGGCTTAAGCGAGGAGATTTTCAGCTCTGTCTCAATCAAGGGATGGGAC	1989
Qy	1900	AGGAAGCTGACTATGGAAGAAGAGAGGCCCAAGAGGATAGCAGAGATGGGAAGCCAGTA	1959
Db	1990	AGGAAGCTTAACAGCCGAGAGAGAGAGGCTCGGAGGATAGCAGAGATGGCCAGCAAGTT	2049
Qy	1960	TTGGGCTAACACCCCAACTTAAGATGATCATTTGAAGAGTCTTATGAGTTCAAGACTACG	2019

[illegible]

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FT CDS 268..3180
FT /*tag= a
FT /product= "Bovine NCX-1 protein"
XX
XX WO200206464-A2.
XX
XX 24-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US21606.
XX
XX 13-JUL-2000; 2000US-218125P.
XX
XX (UMOR ) UNIV MISSOURI.
XX
XX Hale CC, Price EM;
XX
XX WPI: 2002-171806/22.
XX
XX P-PSDB: AAE18291.
XX
XX
XX Producing recombinant proteins e.g. membrane, transport and channel
XX forming proteins in larvae expression system, by infecting larvae with
XX vector having a sequence encoding recombinant fusion protein with
XX affinity tag
XX
XX Example 1: Page 31-37; 40pp; English.
XX
XX The patent discloses methods of producing recombinant proteins in larvae
XX expression system, by infecting the larvae with vector having a sequence
XX encoding recombinant fusion protein with affinity tag. The methods are
XX useful for producing recombinant protein, preferably membrane proteins,
XX transport proteins such as NCX1 (cardiac sodium-calcium exchange protein)
XX or Na-K ATPase, channel forming proteins such as cystic fibrosis trans-
XX membrane conductance regulator (CFTR), junctional protein (connexin 32),
XX receptor, cytoskeletal and other membrane associated proteins. They are
XX also useful for producing prostate specific membrane antigens and sodium
XX phosphate co-transporters from kidney. The methods are also useful for
XX producing recombinant fusion proteins in large quantities that are both
XX highly homogeneous and biologically active. The recombinant proteins
XX produced by the methods of the invention can be included as part of a
XX pharmaceutical, nutritional, drug or vaccine composition. The present
XX sequence is a cDNA encoding bovine NCX-1 protein.
XX
XX Sequence 4087 BP; 1057 A; 950 C; 1057 G; 1023 T; 0 other;
XX
XX Query Match 44.4%; Score 1227.8; DB 24; Length 4087;
XX Best Local Similarity 67.1%; Pred. No. 0;
XX Matches 1935; Conservative 0; Mismatches 777; Indels 171; Gaps 7;
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XX 307 TTTCAAGTGTATGATGATGCTCTCTCTTTTCCCATGTGACCATTAAGTGTCTGAG 366
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XX 106 GGGGACGTGCCAAGCAGACGAGGCAACAATGATCTCTTCAGGGTCATCGAGCTCAAG 165
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 367 ACAGAAATGGAAGAGGAGGCAACAGACTGGGAGTGAAGTCCATTACTGTAAG 426
XX
XX 166 GAGGATGATCTCTGCAATCTGTGTAACCGGAGAACCCCTTCCTTGGGAGCAAGATTGCC 225
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 427 AAGGGGGGTAATTTTACCCATTTTGGGAGCCCGAGGAGCCCTTCCTTGGAGCAAAATTTGCT 486
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XX 226 AAGGTATGTTCTATTTTGTGGCCGTGATATACATGTTCTTGGGGTGTCCATTTGCT 285
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XX 286 GACCGCTTCATGATCTATTGAGTCACTACCTCTCAAGAGAGGAGGTGCAATTTAAG 345
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XX 406 CTGACCTTATGAGCCCTGGGTTCTCTGTCTCTGAGATACCTCTCTTATTTAGAGTG 465

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DB 667 CTGACCTTGATGGCCCTGGGGTCTTACAGTCCAGAGATTTCTCTTCACTAATTCAGAGTG 726
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XX 727 TGTGGCATTAACCTTACTTCAGAGAGACCTTGGCCCTAGACCATCGTGGGAGTGTCTGCA 786
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XX 526 TTCAACATGTTTATCATCATTTGGCATGTGTCTCTAGTGCATCCAGAGGAGAGACTGCG 585
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XX 646 TGGCTCTATATGATTTCTGACACTCTTCCCTGCTGTGTGTCAGGATTTGGAGAGCCCTC 705
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XX 907 TGGCTTTACATCATTTTGTGCTGACGCTCCCTGGGGGTGTGAGAGTCTGGAGAGTTTG 966
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XX 706 CTCACCTCTTCTTCTTCTTCCAGTGTGTCTCTCTGCGCTGGGTCGACATTAAGACTGTG 765
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XX 1027 CTGTTTACAAATATGCTACAGAGATTCGGGCTGCGCAACACAGAGGAAATGATTAAT 1086
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XX 826 GAGACAGAGGTGACACACC-----TAAGGCAATTGAGATGATGCAAAATGATG 876
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XX 1087 GAACAGAGAGGAGAGACGACCTTCCAAAGACAGAAATGAATGATGAGAAAGTGTGTC 1146
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XX 877 AATTCOCATTTTC-----TAGATGGAAACGTGTGCTCCCTGGAAAGGAAAG----- 921
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XX 922 ---GAAGTGGATGATCCCGACAGAGATGATCCGATCTCAAGATCTGAAGCAAAA 978
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XX
XX 1396 GTGGGCAATTAATGATGAGACATTTTGAAGAGATGAAACATCTTCTTGTAAAGTTGAGC 1455
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 1687 GTTGGCATCATGATGATGACATCTTTGAAGAGATGAGAAATTTCTTGTGTGATCTCAGC 1746
XX
XX 1456 AATGTCCGATGAGAGAGAGAGCAGCAGAGAGGAGGATGCCCTCCAGCAATATTTCAACAGT 1515
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

D 1747 AACGTCAAAGTATCTTGGAAAGCCTCGAAGAGCGGACATCTGGAAGC-----CAGT 1797
Q 1516 CTTCCCTTGGCTCGGCGTGTCTTACGCTCCCTGTGTGGCCACAGTTACATCTTGAT 1575
D 1798 CATGTCTCTACCCCTGTGGTGGATGCCCTCCACTGCGACCGGACATTTTGTAT 1857
Q 1576 GATGACCATGAGCGATCTTCTACTTTTGAATGTGATACTATTCATGTGACGAGTAT 1635
D 1858 GATGACCATGCTGCGCATCTTCTACTTTTGAAGAACCGGTGACTCATGTGAGAGAGCAT 1917
Q 1636 GGTGTATGAGGATGAGGATCTGCGGACATGAGTGCGCGGGGTACAGTACGTGCTCC 1695
D 1918 GGCATCTATGAGAGTGAAGTTCTGAGAACATCTGAGACAGTGAAGATGTATCTGTTCC 1977
Q 1696 TTATGACAGTAGAAGGAGACAGCCAGAGGCGGTGAGGACTTTGAAGACATATAGG 1755
D 1978 TATTAAGACCATTTAGGGGAGCCGAGAGGTGAGGGAGACATTTGAGACACATGGGA 2037
Q 1756 GAGTGGATTTCAAGATGATGAAGCTGTGAAGAACATTAAGGTTAAATAGTAGATAG 1815
D 2038 GAGCTCAGATTCAGAAATGAGAAATGTCAAAACATATCAGTCAAGTAAATGATGAT 2097
Y 1816 GAGGATACGAAGAGCGAAGAAATTTCTCATTTGCCCTTGTGAACCGAATGATGG-- 1873
D 2098 GAGGAGTATGAGAAACAAAGACCTTCTCTTGAATGAGAGCCCGCTGTGGAG 2157
Q 1874 -----AACGTGAA 1882
D 2158 ATGATGAGAAAGAACCCCTGTTATTGATGAGCTTGGTGGCTTCAACATTAACAGGAAA 2217
Q 1883 TATCAGATGTGACAGACAG----- 1901
D 2218 TACCTGTATGCGCAGCGCTGTCTTCAAGAAAGTTCATGCTAGAGAACATCCACTCCCTCT 2277
Q 1902 -----GAAAGCTGATATGAGAAAGAG 1923
D 2278 ACTATATCAACCATCGCAGATGATATGATGACAGACGCGCACTGACACAAAGAGAG 2337
Q 1924 GAGGCCAAGAGGATAGCAGAGATGGGAAGCCAGTATTTGGGTGACACCCCAACTAGAA 1983
D 2338 GAAGAGAGGCGCATTTGGGAAATGGGGCGCCCATCTGTGGAGAGCAGACAGCTGGAG 2397
Q 1984 GTGATCATTTGAAGAGTCTTATGAGTTCAAGACTACGCTGACAACTGATCAAGAGACA 2043
D 2398 GTGATCATTTGAAGAGTCTTATGAGTTCAAGAGTCTGACAACTGATTAAGAGACA 2457
Q 2044 AACCTGGCCCTTGGTTGGGGACCAATTCCTTGGAGGAGACATTCATGAGGGCATCAC 2103
D 2458 AACCTAGCCCTCTGTGTGGAGAGAACAGCTGGAGAGACAGTTCAATCGAGGATCACT 2517
Q 2104 GTGAGTGCAGCAGGGGATGAGATGAGATGAATCCGGGAGAGAGAGGCTGCCCTCTGC 2163
D 2518 GTGAGTGTGGGAGATGAGATGAGAGATGAGAGATGAGGAGAGAGAGAGGCTCCCTCT 2577
Q 2164 TTTGATCTAGCTCATGCACTTCTGACTGTCTTGTGAAGGTGCTGTGCTGTGCTG 2223
D 2578 TTTGATCTAGCTCATGCACTTCTGACTGTCTTGTGAAGGTGCTGTGCTGTGCTG 2637
Q 2224 CCCACAGAGTACGCGAGCGCTGGCGCTGGCGGTCCATCCATCATATGTCGATG 2283
D 2638 CCGACAGAGTACGCGAGCGCTGGCGGTGCTGTGATGCTCTCCATCTCATGATGCGCTA 2697
Q 2284 CTCACGCGCATTTGGGAGACCTGCGCTGCACTTGGCTGCAACATTTGGTCTCAAGAT 2343
D 2698 CTCACGCGCATTTGGGAGACCTGCGCTGCACTTGGCTGCAACATTTGGTCTCAAGAT 2357
Q 2344 TCAGTACAGCTGTGTTTTCGTGGCATTTGGCAGCTCTGTGCCAGATAGCTTGGCAG 2403
D 2758 TCCGTACCGCGGTGTGTGTGCTGGCTTGGAACTCAGTCCAGACATATTTGCAAGC 2817
Q 2404 AAAGTGTGCGCTTCAGAGATGTATATGAGAGCGCTCATTTGGGAGAGCGGAGGCGCAG 2463
D 2818 AAAGTGTGCGCTTCAGAGATGTATATGAGAGCGCTCATTTGGGAGAGCGGAGGCGCAG 2877

Q 2464 AACGCGGTCAATGTCTTCTGCGGATCGGCTGGCTGTCCGTCGCGCCCATCTAGG 2523
D 2878 AACGCGGTGAAGCTTCTTCTGCGGATCGGCTGGCTGTCCGTCGCGCCCATCTAGG 2937
Q 2524 GCTTCTGAGGAGACAGAGTTCACAGTGTGGCGCGACACATGCGCTTCTGCTACCTC 2583
D 2938 GCGGCCAACGCGGGAACATTCAAAGTGTCCCTGCGACGCTACCTTTTCTGTACCTC 2997
Q 2584 TTACCATCTTTGATTTGCTGATCAGGCTGCTGTGACGGAAGGCGCGGACCTG 2643
D 2998 TTACCATCTTTGCTTTCATCATATGAGGCTGCTGTGATGCGCGGAGCGAGAAAT 3057
Q 2644 GAGGCGGAGCTTGGTGGCGCCCGCTGCTGCAAGCTGCGCACAAACATGCTTTTGTGAGC 2703
D 3058 GAGGATGAGCTGGGTGGCGCCGACAGCTGCGCAAGCTCTCATATCTGCTTTGTGCTC 3117
Q 2704 CTGTGCTCTCTTACATATCTTCTTGGCCACATGAGGCTTATTTGATCAATCAAGGGTTC 2763
D 3118 CTGTGCTCTTGTACATTTCTTCTCTCTCTGAGGCGCTACTGCGCACATAAAGGCTTC 3177
Q 2764 TAA 2766
D 3178 TAA 3180

RESULT 7

ABV24305
ID ABV24305 standard; cDNA: 5438 BP.

AC ABV24305;

DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 24296.

DE Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX Homo sapiens.

PN WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001MO-US05171.

PF 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PA Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

CC prostate cells and correlating with presence of prostate cancer, useful

CC for detecting presence of prostate cancer, stage of prostate cancer -

XX Claim 1: Page 4554-4555; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
Sequence 5438 BP; 1526 A; 1110 C; 1276 G; 1520 T; 6 other:
50
Query Match 43.7%; Score 1208.8; DB 23; Length 5438;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 762; Indels 171; Gaps 5;
QY 109 GACGTGCCAAGCAGGCGAGACATGATCTCTTCAGGCTATCGGATCGCAAGG 168
DB 245 GAAATGGAGGAGGAAATGAAATGATGATGATGATGATGATGATGATGATG 304
QY 169 GGTGTCATCTGCTCAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 228
DB 305 GGGGTGATTTTGGCCATTTGGGAGACCCGATCTTTTGGGAGCAAAATTTGCTGA 364
QY 229 GTGATTTGCTATTTTGTGGCCCTGATATACATGTTCTTGSGGTGTCATCATTTGCTGAC 288
DB 365 GCTACTGTGATTTTGTGGCCATGCTACATGTTCTTGAGTCTCATATCATACTGAT 424
QY 289 CGCTTCATGACATCTATTTAGATGATCACCCTCTCAAGAGGAGGAGTGAATTAAGAA 348
DB 425 CGGTTCATGCTCTCTATGAAAGTATCATCATCTCAAGAAAAAATTAACATTAAGAA 484
QY 349 CCCATGGAAGAACAGACACACCACTATGCGGTCTGGAATGAAGTCTCCCAACCG 408
DB 485 CCCAATGGAGAGACACCAACAGCACTGAGAGATCGAAATGAACATTTCTCAACCG 544
QY 409 ACCCTTATGGCCCTGGTTCCTCTCTCTGATGATCTCTCTTAAATTTAGGTTGT 468
DB 545 ACCGTGATGGCCCTGGGATCTTCTCTCTGATTTCTCTTCAATTAAGTGTGT 604
QY 469 GGTGATGGGCTGATCTGCTGATGATGAGACCTTCTACATTTAGAGAGTCAAGCTTC 528
DB 605 GGCCTTAATCTTCTGAGAGAGACCTGCTCTACACCATGCTGGAAGTCTCTCATTC 664
QY 529 AACATGTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 588
DB 665 AATATGTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 724
QY 589 ATCAAGCATCTACGATCTCTCTTCAACACCGCTGCTGAGATCTTTGCTCAACATCTG 648
DB 725 ATTAAGCATTTGCGTCTCTCTTGTGACAGACGCTGAGCATCTTTGCTCAACATCTG 784
QY 649 CTCTATATGATTTGCGAGCTCTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
DB 785 CTCTATATGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 844
QY 709 ACT 768
DB 845 ACTTCT 904
QY 769 TTCTCAAAATACATCACAAGAAATACGACAGACAAACCGAGATTTATCATATAG 828
DB 905 TTTTCAAGATATGCTACAGAGATATGAGTGGCAACAGAGGGGATATTTATGAA 964
QY 829 ACAGAGGTGACACCC-----TAAGGCAATTGAGATGATGAGAAATGATGAT 879
DB 965 CATGAGAGAGACAGCATCTTCTAAGACTGAATTAAGAAAGAGGAAAGTGTGCAAT 1024
QY 880 TCCCATTTTCTAGATGGGAACCTGGTGGCCGGAAGGAG----- 921
DB 1025 TCTCATGTTGAAATTTCTTATGATGCTGCTGCTGCTGAGAGTGAAGAGGACCA 1084
QY 922 GAAGTGAATGATCCCGCAGAGAGATGATCCGATTTCTCAAGATCTGAAGCAAAACAC 981

DB 1085 GATGATGAAGAAGCTAGGCGAGAAATGGCTAGATTTCTGAAGAACTTAAGCAGAAGCAT 1144
QY 982 CCAGGAAAGGACTTAGATCAGTGTGTGAGATGGCCATTTACTATGCTCTTTCCACCA 1041
DB 1145 CCAGTAAAGAAATAGACAAATTAATTAAGTAACTACCAAGTCTTAAGTAGAGAG 1204
QY 1042 CAGAGAGCGCGCTTACCGATTCAGGACGATGATGATGATGATGATGATGATGATG 1101
DB 1205 CAAAAAGTAGAGCATTTTATTCGATTCAGCTACTCCGCTCATCTAGCTGAGCTGGCA 1264
QY 1102 ATCTGAAGAAATCAGCAGACAGACAGCAAGAGGCTCCAGCATGAGCGAGTGCAC 1161
DB 1265 ATTTTAAAGGACATGAGCTGACAGAGCAAGAGGCTGTCAGATGACGAGAGTCAAC 1324
QY 1162 ACCGATGAGCTG---AGACCTTTATTTCCAAAGCTCTTTGACCACTGTTCTTACAG 1218
DB 1325 ACTGAAGTACAGAAAGAACCCCTGTGTAGATCTCTTTGAACAAAGGCAATATCAG 1384
QY 1219 TGCTGAGAACTGTGGGCTGTACTCCTGACAGTGTGTGAGAAAGGGGAGACATGTCA 1278
DB 1385 TGTCTGAGAACTGTGTGATCTGTGGCCCTTACCATTTATCCGAGAGTGTGATTTGACT 1444
QY 1279 AAGACCATGTATGTGACTACAAACAGAGATGCTTCCCAATGACAGGCGTGCATAT 1338
DB 1445 AACCTGTGTTTGTGACTTACAGAAAGAGATGAGCAAGAAATGCTGCTGCTATATAT 1504
QY 1339 GAGTTCACAGAGGACGCTGTCTGAAAGCCAGAGAGACCCCAAGAGATTTCTCCGTG 1398
DB 1505 GAATTTACTGAAGGAAGTGTGTGTTAAGCTGTGTATACCAAGAAATTCAGAGTG 1564
QY 1399 GGCATATGATGAGACATTTTGTGAGAGATGAACATCTTTGTAAGTTGATGCANT 1458
DB 1565 GGTATCATATGATGATGATATCTTTGAGAGAGATGAATAATTTCTTGTGATCTCAGCA 1624
QY 1459 GTCCCATGAGAGAGAGACAGCAGAGAGAGGATGCTCCACAAATATTTCAACAGTCT 1518
DB 1625 GTCAAGATCTTCTGAAAGCTTACAGAAAGTGCATATCTGAAAGC-----CATCAT 1675
QY 1519 CCCTTGTGCTGGGCTGTCTTACCTCCCTTGTGTGAGCCACAGTTTACATCTTGTGATG 1578
DB 1676 GTTTTACACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1735
QY 1579 GACCATGACGATCTTCTTGAATGATGATGATGATGATGATGATGATGATGATG 1638
DB 1736 GACCAAGGAGGATTTTATCTTTGAGAACCTGTGACTCATGTGATGAGACATTTGCC 1795
QY 1639 GTTATGAGGTCAGAGTCTGCGGACATCAGTGTGCGGAGTACAGTCACTGCTCCCTT 1698
DB 1796 ATCATGAGAGTGAAGTATTTGAACATCTGAGAGCTCGAGAAATGTTATGTTCCATAT 1855
QY 1699 AGGACATGAGAGGAGACAGCAGAGGCTGCGGTGAGAGCTTTGAAGACACATATGGGAG 1758
DB 1856 AAAACCATGAGAGGAGCTGCGAGAGTGAAGGAGGATTTTGAAGACACTTGTGAGAG 1915
QY 1759 TTGGAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1818
DB 1916 CTGCAATTTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1975
QY 1819 GAATACGAAGGACAGAGATTTCTTCAATTTGCCCTTGTGAACCGAATGATGAGAA--- 1875
DB 2036 AGTGAAGAAAGAGCCCTGTTATTTGAATGAGCTTGTGCTTCAATAACAGAAAAATAC 2095
QY 1876 ----- 1875
DB 2096 CTGTTTGGCCAACTGTCTTCAAGAGGTTTCAATGCTAGAAACATCCGATTTCTCTACT 2155
QY 1876 -----CGTGAATATCAGATGTGACAGACAGAGAGCTGATATGAGAAAGAGAG 1926
DB 2156 GTATATCACCATTGACAGCAATATGATGACAGAGCCACTGACAGCAAAAGAGAGAG 2215

Db 493 COTGAGGAGACAGTTTCATGAGAGCCATACCCGTGATGTCAGAGGAGGATGAGATGAG 552
Qy 2132 ATGAATCCGGGAGAGAGGCGCCCTGCTTGTAGTACGTATGACATCCGACATG 2191
Db 553 ATGAATCCGGGAGAGAGGCGCCCTGCTTGTAGTACGTATGACATCCGACATG 612
Qy 2192 TCTTCTGGAAGAGTGTGTTTGGCCCTGTGTCGCCCCACAGAGTACTGCCACGGCTGGGCT 2251
Db 613 TCTTCTGGAAGAGTGTGTTTGGCCCTGTGTCGCCCCACAGAGTACTGCCACGGCTGGGCT 672
Qy 2252 GCTTGGCCGTCTCCATCCTCATCATATGGAGTGTACCGGCCATCATTTGGGAGCTGGGCT 2311
Db 673 GCTTGGCCGTCTCCATCCTCATCATATGGAGTGTACCGGCCATCATTTGGGAGCTGGGCT 732
Qy 2312 CGCACTTGGGCTGCACATTTGGTCTCAAAAGTTCAGTACAGTCTTGTGTTTCGGTGCAT 2371
Db 733 CGCACTTGGGCTGCACATTTGGTCTCAAAAGTTCAGTACAGTCTTGTGTTTCGGTGCAT 792
Qy 2372 TTGGCAGCTCTGTCCCAATACGTTTGGCAGCAAGTGTGCTCCCTCCAGATGTATATG 2431
Db 793 TTGGCAGCTCTGTCCCAATACGTTTGGCAGCAAGTGTGCTCCCTCCAGATGTATATG 852
Qy 2432 CAGACGCTCCATTTGGCAACGTGACGGGAGCAACGCCGTCAATGTCTTCTGGGCAATCG 2491
Db 853 CAGACGCTCCATTTGGCAACGTGACGGGAGCAACGCCGTCAATGTCTTCTGGGCAATCG 912
Qy 2492 GCTTGGCCGTCTCCATCCTCATCATATGGAGTGTACCGGCCATCATTTGGGAGCTGGGCT 2551
Db 913 GCTTGGCCGTCTCCATCCTCATCATATGGAGTGTACCGGCCATCATTTGGGAGCTGGGCT 972
Qy 2552 CGGCGGAGACACTGGCTTCTTCCGTCACGCTTTCACCATCTTTGATTTGTCTGATCA 2611
Db 973 CGGCGGAGACACTGGCTTCTTCCGTCACGCTTTCACCATCTTTGATTTGTCTGATCA 1032
Qy 2612 GCGTGTCTTGTATCCGAAGGCGCGCACCTGGAGGAGGAGCTTGTGGCCCGCTGTGCT 2671
Db 1033 GCGTGTCTTGTATCCGAAGGCGCGCACCTGGAGGAGGAGCTTGTGGCCCGCTGTGCT 1092
Qy 2672 GCAGGCTGGCCACACATGGCTTGTGTGAGCTGTGGCTCTCTACATACCTTTTGCA 2731
Db 1093 GCAGGCTGGCCACACATGGCTTGTGTGAGCTGTGGCTCTCTACATACCTTTTGCA 1152
Qy 2732 CACTAGAGGCTATGTATCATCAAGGGTTCTAA 2766
Db 1153 CACTAGAGGCTATGTATCATCAAGGGTTCTAA 1187

RESULT 9
ABAg4480
ID ABAg4480 standard; DNA: 1836 BP.
XX
AC ABAg4480;
XX
01-FEB-2002 (first entry)
DT
XX Human foetal liver single exon nucleic acid probe #12785.
DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
FN W0200157277-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver -
XX
PS Claim 4: SEQ ID NO 12785; 639pp + sequence listing; English.
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;

Query Match 28.5%; Score 787.2; DB 22; Length 1836;
Best Local Similarity 68.3%; Pred. No. 3,9e-216;
Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

Qy 109 GAGGTGCCAAGACAGAGGAGCAATGATGCTGTTCAGGTCATCGGACTGCAAGAG 168
Db 133 GAAATGGAAGAGGAAGGAATGAACTGATGATGATGATGATGATGATGATGATGATG 192
Qy 169 GGTGTATCTCCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 228
Db 193 GGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 252
Qy 229 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 288
Db 253 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
Qy 289 CGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 348
Db 313 CGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 372
Qy 349 CCCAATGGAAGAACCAACCACTATGCGGTGTGGAATGAACCTGTCCAACTG 408
Db 373 CCCAATGGAAGAACCAACCACTATGCGGTGTGGAATGAACCTGTCCAACTG 432
Qy 409 ACCCTTATGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTG 468
Db 433 ACCCTTATGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTG 492
Qy 469 GGTGATGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCG 528
Db 493 GGTGATGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCGGTGTGCG 552
Qy 529 AACATGTTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 588
Db 553 AACATGTTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 612
Qy 589 ATCAAGCATCTAGAGATCTTCTTCAACACCGGTGTGGAAGTATCTTTGCTTCAATCTG 648
Db 613 ATTAAGCATCTAGAGATCTTCTTCAACACCGGTGTGGAAGTATCTTTGCTTCAATCTG 672
Qy 649 CTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708
Db 673 CTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 732
Qy 709 ACTGCT 768
Db 733 ACTGCT 792


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QY 769 TTCTCAAAATACATGCACAAAAGTACCGACAGACAAACCGAGGAATTATCATAGAG 828
  || || || || || || || || || || || || || || || || || || || || || ||
Db 793 TTTTACAAAGATATGCTACAAAGAGTATCGAGCTGGCAAGAGAGGGGATGATTATTGAA 852
QY 829 ACAGAGGGTACCCACCC-----TAAGGCATTGAGATGATGGGAAATGATGAAT 879
  || || || || || || || || || || || || || || || || || || || || || ||
Db 853 CATGMAAGAGACAGGCCATCTTCTMAAGCATGMAATTGMAATTGACGGGAAAGTGCTCAAT 912
QY 880 TCCCATTTTGTAGATGGGAACCTGTCGCCCTCGAAGGSAAG----- 921
  || || || || || || || || || || || || || || || || || || || || || ||
Db 913 TCTCATTTTGAATAATTTTCTTAGATGCTGCTCTGCTTGGAGGTGGATGAGAGGACCAA 972
QY 922 GAAGTGTAGATGCCCGACAGAGATGATCCGATTTCTCAAGATCTGAAGCAAAAACAC 981
  || || || || || || || || || || || || || || || || || || || || || ||
Db 973 GATGATGAAGAGCTAGCGCGAAGAAATGGCTAGATCTGAGAGAACTTAAGCAGAACAT 1032
QY 982 CCAGAGAAAGACTTATGATCAGCTGTGTGAGATGGCCAACTATGCTCTTTCCACCAA 1041
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1033 CCAGATTAAGAAATAGACATTAATTAATTAAGCTAACTACCAAGTCTTAAGTCACAG 1092
QY 1042 CAGAAAGCCGCGCTTCTACCGGTATCCAGGCCACCTGATGATGATGGTGGAGCAAT 1101
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1093 CAAAAGATAGAGCATTTTATTCGATTCAGACTACTGCTCATGACTGGAGCTGGCAAC 1152
QY 1102 ATCTCTAAGAAACATGCGAGAGAAACAAGAGCGCTCCAGCATGAGCGAGGTGCAC 1161
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1153 ATTTTAAAGAGCATGTGACGACCAAGCAAGAAAGCTGTACAGCATGACGAGAGTCAAC 1212
QY 1162 ACCGATAGAGCTG---AGGACTTATTTCCAAAGTCTTCTTTGACCATGTTCTTACCAG 1218
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1213 ACTGAATGACTGMAAATGACCCCTGTAGTAAATCTTCTTGAACAAAGGACATATACAG 1272
QY 1219 TGCCTGAGAACTGTGGGCTGTACTCTGACATGATGCTGAGAAAGGGGAGACATCTCA 1278
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1273 TGTCTGAGAACTGTGTACTGTGCGCTTACCTTATCCGACAGAGTGGTGAATTTACT 1332
QY 1279 AAGACCATGTATGTGACTACAAAACAGAGATGCTTCTCCAAATGACAGGGGCTGACTAT 1338
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1333 AACACTGTGTTGTGACTTACAGAACAGAGATGGACACAAATGCTGGGTCTGATTAAT 1392
QY 1339 GAGTTCACAGAGGACAGGTGTCTGAAGCCAGAGAGACCCAGAAAGAGTCTCCGTG 1398
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1393 GAATTTACTAAGGAACTGTGGTGTAAACCTGTGTATACCCAGAAAGAAATCAGAGTG 1452
QY 1399 GGCATTAATGATGACGACTTTTGTGAGAGATGAAACATCTTGTAAAGTTGAGCAAT 1458
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1453 GGTATCTATATGATGATGATCTTTGAGAGAGATGAATAATTTCTTGTGCACTTCAGCAAT 1512
QY 1459 GTCCGATAGAGAGAGACAGCCAGAGAGGGGATGCTCCAGCAATATTTCAACAGTCTT 1518
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1513 GTCAAAAGTATCTTCTGAAAGCTTACAGAGATGGCATTAAGTGAAGC-----CAATCAT 1563
QY 1519 CCCCTGCTGGGCTGTCTCAGAGCTCCCTTGTGTGCGCCACAGTATACATCTTGATGAT 1578
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1564 GTTCTTAACACTTCTGCTCCGATCTCCGATCTCCACACTGCACTGTAATTTTGTAGAT 1623
QY 1579 GACCATCAGAGCACTCTCACTTTTGAATGTATCACTATGATGATGAGAGATGTGT 1638
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1624 GACACAGCAGAGCACTTTTACTTTTGAAGAACTGTGACTATGATGATGAGAGATGGC 1683
QY 1639 GTTATGAGAGTCAAGGTTCTGCGACATCAGGTGCCCGGGGTACAGATCAGTCCCTTT 1698
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1684 ATCTATGAGGTGAAGATTTGAGAACATCTGAGAGCTCGAAGAAATGTTATCTTCCATAT 1743
QY 1699 AGGACAGTAAAGAGGACAGCCAAAGGTGGCGGTGAGAGACTTTGAAGACACATATGGGAG 1758
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1744 AAAACCACTCAAGGAGACTGCGCAGAGGTGAGGGAGGATTTTGAAGACACTGTGGAGAG 1803
QY 1759 TTGGAATTCAGAAGATGTAACGTGAAA 1788
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1804 CTGGAATTCAGAAGTGAAGAAATTTGTAA 1833
```

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RESULT 10
ID ABA31619
AC ABA31619 standard; DNA; 1836 BP.
XX
AC ABA31619;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #10085 for gene expression analysis in human heart cell sample.
XX
KW Human: gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR:
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
PS Claim 4; SEQ ID NO 10085; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;
XX
Query Match 28.5%; Score 787.2; DB 22; Length 1836;
Best Local Similarity 68.3%; Pred. No. 3.9e-216;
Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;
QY 109 GAGTGGCAAGCAGCAGGGGAGAGAAATGAGTCTCTGTTCAGAGGTATCGACTGCAAGAG 168
  || || || || || || || || || || || || || || || || || || || || || ||
Db 133 GAATATGAGAGAGAGAGAAATGAAATGAGATGCTACTGATCATATTAATTAAGAA 192
QY 169 GGTGTCTATCTGCCAATCTGTGATCCCGAGAACCTTCCCTTGGGACAAAGATTGCCAGG 228
  || || || || || || || || || || || || || || || || || || || || || ||
Db 193 GGGGTGATTTTGGCCATTGGGAACCCCAAGACCTCTTTTGGGGCAAAATTTGCTAGA 252
QY 229 GTATCTCTATATTTTGGGCGCTGATATATATGCTTGGGGTGCATCATTCATGCTGAC 288
  || || || || || || || || || || || || || || || || || || || || || ||
Db 253 GCTACTGTATATTTTGGGCGATGCTATCATATTTTGGGATCTTATCATAGCTGAT 312
QY 289 CGCTTCATGCACTATTAAGTCAATCACCCTCAAGAGAGGAGGACAAATTAAGAAA 348
```

Db 313 CGGTTCATGTCCTCTATAGAAATCATCATCTCAAGAAAAAATAACCTTAAGAAA 372
Qy 349 CCCAATGAGAAACAGACACAACACTATTGGGCTCGGAATGAACCTGTCCAACTG 408
Db 373 CCCAATGAGAGACACCAACAGCAACTGTGAGATCTGAAAGAAAGTTCTTAACCTG 432
Qy 409 ACCCTTATGGCCCTGGTTCCTGCTCTGATGATCTCTTATATGAGTGTG 468
Db 433 ACCTTGATGGCCCTGGGATCTTCTGCTGATTTCTCTTCACTTATGAACTGTG 492
Qy 469 GGTCAATGGGTTCACTGCTGATCTGATCTGATCTTCACTTATGAGGATCTG 528
Db 493 GGCCTAATCTTCACTGAGAGAGACTCGGTCTTACACCATGCTGGAAGTCTGATTC 552
Qy 529 AACATGTTCAATCATTTGGCATCTGTGTCTACGTGATCCAGAGAGAGATCGCAAG 588
Db 553 AATATGTTCAATCATTTGATGATCTGATGATGATGATGATGATGATGATGATG 612
Qy 589 ATCAAGCATCTACGATCTGCTCTATCAACCGCTGCTGAGATCTGCTGATCTG 648
Db 613 ATTAAGCATTTGCGTCTCTCTTGTGACAGAGAGCTGAGCATCTTGTCTTACCTG 672
Qy 649 CTCTATATGATTTGCGAGATCTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
Db 673 CTCTATATTTTGTCTGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Qy 709 ACT 768
Db 733 ACT 792
Qy 769 TTCTCAATATCATGACAAAAAGTACGACAGACAAACCGAGGATTTATCATAG 828
Db 793 TTTTCAAGTATGTTTACAGAGATGATGAGCTGCAAGAGAGGAGGATTTATGAA 852
Qy 829 ACAGAGGCTGACACACC-----TAAGGCTATGATGATGATGATGATGATGAT 879
Db 853 CATGAAGAGAGACAGGCACTCTCTAAGACTGAAATTTGAATGAGAGGAAATGCTCAT 912
Qy 880 TCCATTTTCTAGATGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
Db 913 TCTCATGTTGAAATTTCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
Qy 922 GAGGAGATGATGCTCCGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 981
Db 973 GATGATGAGAGCTAGGAGAGAAATGCTGATGATGATGATGATGATGATGATGAT 1032
Qy 982 CCAGAGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1041
Db 1033 CCAGATTAAGAAATAGAGCAATTAATAGATTAATAGATTAATAGATTAATAGAT 1092
Qy 1042 CAGAGAGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
Db 1093 CAAAAAATAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1152
Qy 1102 ATCTGAG 1161
Db 1153 ATTTAAAG 1212
Qy 1162 ACCGATGAG 1218
Db 1213 ACTGAAG 1272
Qy 1219 TGCTGAG 1278
Db 1273 TGCTGAG 1332
Qy 1279 AAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
Db 1333 AACACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1392
Qy 1339 GAGTTACAG 1398

Db 1393 GAATTACTGAG 1452
Qy 1399 GGCATATTTGATGAG 1458
Db 1453 GGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512
Qy 1459 GTCCGATGAG 1518
Db 1513 GTCAAGATTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1563
Qy 1519 CCCTTGCTGAG 1578
Db 1564 GTTCTGAG 1623
Qy 1579 GACCATGAG 1638
Db 1624 GACCAAG 1683
Qy 1639 GTTATGAG 1698
Db 1684 ATCATGAG 1743
Qy 1699 AGGACAGTGAAG 1758
Db 1744 AAACCATGAG 1803
Qy 1759 TTGGAATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1788
Db 1804 CTCGAAATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833

RESULT 11
AAK12937
ID AAK12937 standard; DNA: 1836 BP.
XX
XX AAK12937;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX
DE Human brain expressed single exon probe SEQ ID NO: 12928.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 12928; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.

XX Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;

Query Match 28.5%; Score 787.2; DB 22; Length 1836;
Best Local Similarity 68.3%; Pred. No. 3.9e-216;
Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

QY 109 GAGGTGCAAGCAGAGGAGGAGCAATGAGTCCCTGTCAGGGTCATCGACATGCAAGAG 168
DB 133 GAATGAGAGAGAGAGAAATGAAACTGTAATGATGATGATGATGATGATGATGATGAT 192
QY 169 GGTGTATCTCTGCAATCTGTGACCGGAGAACCCCTTCCCTGGGACAAAGATTGCCAG 228
DB 193 GGGGTGATTTTGGCCATTTTGGAAACCCCAAGACCCTTCTTTGGGGACAAATTTGCTAGA 252
QY 229 GTGATGTCATTTTGGGCGCTGATATGATGTCCTTGGGGTCATCATGATGATGATGAT 288
DB 253 GCTACTGTGATTTTGGGCGCTGATGATGTCCTTGGGGTCATCATGATGATGATGATGAT 312
QY 289 CGCTTCATGCAATCTATGAGATCATACCTCTCAAGAGAGGAGGATGACATTAAGAAA 348
DB 313 CGGTGATGTCCTCTATAGAAATGATCATCATCAAGAAAGAAATTAACATTAAGAAA 372
QY 349 CCCAATGAGAAACCAAGCAGACCAATATGCGGTCTGAGATGAACTGTCTCCACCTG 408
DB 373 CCCAATGAGAAACCAAGCAGACCAATATGCGGTCTGAGATGAACTGTCTCCACCTG 432
QY 409 ACCCTTATGCGCGGTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 468
DB 433 ACCCTTATGCGCGGTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 492
QY 469 GGTGATGAGGTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
DB 493 GGGCATATCTTCACTGAGAGACCTGCGTCTAGACACATCGTGGAAAGTCTGATCTG 552
QY 529 AACATGTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
DB 553 AACATGTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 612
QY 589 ATCAAGATCATGAGAGCTTCTGATCAGCGGCTTGGAGTATCTTGGCTATCATGATG 648
DB 613 ATCAAGATCATGAGAGCTTCTGATCAGCGGCTTGGAGTATCTTGGCTATCATGATG 672
QY 649 CTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
DB 673 CTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 732
QY 709 ACT 768
DB 733 ACT 792
QY 769 TTTTACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 828
DB 793 TTTTACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 852
QY 829 ACAAGAGGTGACCAACC-----TAAGGCAATGATGATGATGATGATGATGATGATGAT 879
DB 853 CATGAAGAGAGAGAGGATCTCTTAAGATGATGATGATGATGATGATGATGATGATGAT 912
QY 880 TCCCATTTTCTAGATGAGAACTGTGTCCTCTGAGAGGAG-----921
DB 913 TCTCATTTTGAATTTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 972
QY 922 GAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 981
DB 973 GAT 1032

QY 982 CCAGAGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1041
DB 1033 CCAGATTAAG 1092
QY 1042 CAG 1101
DB 1093 CAAAG 1152
QY 1102 ATCCGTAAG 1161
DB 1153 ATTTTAAG 1212
QY 1162 ACCGATGAGCTG--AGACTTATTTTCCAGAGCTCTTGTGACCATGTTCTTACAG 1218
DB 1213 ACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1272
QY 1219 TGCTGAG 1278
DB 1273 TGCTGAG 1332
QY 1279 AAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
DB 1333 AACACTGTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1392
QY 1339 GAGTTTCAAG 1398
DB 1393 GAATTTTCAAG 1452
QY 1399 GGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1458
DB 1453 GGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512
QY 1459 GTCCGATGAG 1518
DB 1513 GTCAAGATATCTTGTGAG 1563
QY 1519 CCTTGGCTGAG 1578
DB 1564 GTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
QY 1579 GACCATGAG 1638
DB 1624 GACCATGAG 1683
QY 1639 GTTATGAG 1698
DB 1684 ATCATGAG 1743
QY 1699 AGCAGATGAG 1758
DB 1744 AAACCATGAG 1803
QY 1759 TTGGAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1788
DB 1804 CTGCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833

RESULT 12
AA119464
ID AA119464 standard; DNA: 1836 BP.
XX
AC AA119464:
XX
XX
DT 12-OCT-2001 (first entry)
DE Probe #9397 for gene expression analysis in human cervical cell sample.
XX
XX Probe: human; microarray; gene expression; cervical epithelial cell;
KM cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.

XX 09-AUG-2001.
PD 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 9397; 487bp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcf_sequences.
XX
SQ Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;

Query Match 28.5%; Score 787.2; DB 22; Length 1836;
Best Local Similarity 68.3%; Pred. No. 3.9e-216;
Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

QY 109 GAGCTGCCAAGCAGGAGGAGAAATGATGCTCTTCAAGGTCATCGAGTCGAAGAG 168
DB 133 GAAATGGAGAAGGAAGGAATGAATGATGATGATGATGATGATGATGATGATGATG 192
QY 169 GGTGTATCTCTGCAATCTGTACCCGGAACCTTCCCTTGGGAGCAAGATTGCCAGG 228
DB 193 GGGGTGATTTTCCCATTTTGGGAACCCCAAGACCTTTCTTTGGGGAAGAAATTTGCTAGA 252
QY 229 GTCATTTGCTATTTTGGCCCTGATATGATGATGATGATGATGATGATGATGATGATG 288
DB 253 GGTACGTGTATTTTGGCCATGCTGATGATGATGATGATGATGATGATGATGATGATG 312
QY 289 GCGTCATGAGCATATTTAAGTATCACCCTCAAGAGAGAGAGTGAATTAAGAA 348
DB 313 CGGTTCATGCTCTTATAGATCATCATCTCAAGAAAGAAATTAACATTAAGAA 372
QY 349 CCCAATGGAGAAACGACCAACACTATTCGGGTCTGGAATGAACCTGCTCAACCTG 408
DB 373 CCCAATGGAGAGACCAACGACCAACTGTGAGATCTGGAATGAACAGTTCTTAACCTG 432
QY 409 ACCCTTATGAGCCCTGGGTCTCTGCTGCTGAGATACCTCTCTTATTTAGAGTGTGT 468
DB 433 ACCCTTATGAGCCCTGGGTCTCTGCTGCTGAGATACCTCTCTTATTTAGAGTGTGT 492
QY 469 GGTCAATGGGTCTGCTGCTGATCTGGGACCTTTCACATTTAGAGTGAAGCTTC 528
DB 493 GGCCTAATCTTCACTGAGAGAGACCTCGGTCTAGACCATGCTGGGAAGTGTGATTC 552
QY 529 AACATGTTTCATCATTTGGCATCTGTGTCTAGCTGATCCAGACGAGAGATCGCAAG 588
DB 553 AATATGTTTCATCATTTATTCACACTGTGTGTTATGTGCTGCTGAGACGAGAGACAAAG 612

QY 589 ATCAAGCATCTACGAGTCTCTTCAATCACCGCTGCTGAGATGCTTTGCCATCTCG 648
DB 613 ATTAAGCATTTCCGTGTCTCTTTGTGACAGAGACCTGGAGATCTTTGCCATCTCG 672
QY 649 CTCTATATGATTTGGCAGCTCTTCCCTGGTGTGTCACAGTTTGGAGAGCCCTCTC 708
DB 673 CTTCATATTTATTTGTGTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
QY 709 ACTCTCTCTCTTTTCCAGTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
DB 733 ACTCTCTCTCTTTTCCAGTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
QY 769 TTCTCAATATACATGACCAAAAGTACCGCAGACAGCAACACGAGATTTATCATAG 828
DB 793 TTTTCAAGTATGCTCTACAGAGTATCGAGCTGGCAGCAGAGGGGATGTTATGAA 852
QY 829 ACAGAGGGGTGACACCC-----TAAAGCATTTGATGATGATGATGATGATGAT 879
DB 853 CATGAAGGAGACAGGCATCTTAAGACTGAATTTGAATGAGAGGGGAAAGTGTCAAT 912
QY 880 TCCCATTTTCTGATGAGGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
DB 913 TCTCATGTTGAAATTTCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972
QY 922 GAAGTGATGATGCCCGCAGAGAGATGATCCGATTTCTCAAGATCTGAAGCAAAACAC 981
DB 973 GATGATGAAGAGCTAGAGCGAAGATGCTAGGATTTCTAAGCAACTTAAGCAAGAACT 1032
QY 982 CCAGAGAAAGACTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1041
DB 1033 CCAGATTAAGAAATGAGCAATTAATAGAAATTAAGTAACTTACCAAGTCTTAAGTACG 1092
QY 1042 CAGAGAGCCCGGCTTCTACCGTATCCAGGACATCTGATATGATGATGATGATGATGAT 1101
DB 1093 CAAAAAGTAGAGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1152
QY 1102 ATCTGGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1161
DB 1153 ATTTTAAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1212
QY 1162 ACCGATGACCTG---AGGACTTATTTCCAAAGTCTTCTTGGACCATGTTCTTAACAG 1218
DB 1213 ACTGAAGTACGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272
QY 1219 TGCCTGAGAACTGTGGGCTGTACTCTGACAGAGTGTGAGAGAGAGAGAGAGAGAGAG 1278
DB 1273 TGTCTGAGAACTGT 1332
QY 1279 AAGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
DB 1333 AACACTGT 1392
QY 1339 GAGTTTACAGAGAGGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1398
DB 1393 GATTTTACAGAGAGGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1452
QY 1399 GGCATATTTGATGACACATTTTGTGAGAGATGAACACTTCTTTTAAAGTTGAGCAAT 1458
DB 1453 GGCATATTTGATGACACATTTTGTGAGAGATGAACAAATTTCTTTGATCTCAACACT 1512
QY 1459 GTCCGATGAG 1518
DB 1513 GTCAAAAGTATCTTGTGAAGCTTCAAGAGATGCAATCTGGAAGC-----CAATCAT 1563
QY 1519 CCTTGGCTCTGGGCTGTCTAGACCTCCCTTGTGTGCCACAGTATACATCTTGTGATGAT 1578
DB 1564 GTTTTACACTTGTCTGCTCGGATCTCCCTCCACAGTATACATCTTGTGATGATGAT 1623
QY 1579 GACCATGACGAGATCTTCACTTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1638
DB 1624 GACCAAGCAGAGATTTTCTTGTGAGAACTGTGACATCATGTGATGAGAGATTTGGC 1683
QY 1639 GTTATGAGAGTCAAGGTTCTGGGAGATCAAGGTCCTCGGGGATCAAGTATCGTCCCTTT 1698

Db 1333 AACACTGTTGTTGACTTTCAGAACAGAGATGGCACAGCAAAATGCTGTCGATTAAT 1392
 Oy 1339 GAGTTCACAGAGGAGGACGGTGTCTGAAAGCCAGAGAGAGCCAGAGAGTCTCCGCG 1398
 Db 1393 GAATTTACTGAAGGAACTGTGTGTTAAAGCTGTGATACCCAGAGAAATTCAGAGTG 1452
 Oy 1399 GGCATTAATTTGATGACACATTTTGTAGAGAGATGAACACTTCTTTGTAAAGTTGAGCAAT 1458
 Db 1453 GGTATCATAGATGATGATATCTTTGAGAGAGATGAATAATTTCTGTGATCTCAGCAAT 1512
 Oy 1459 GTCCGCATAG 1518
 Db 1513 GTCAAGATATCTTCTGAAGAGCTTCAGAAAGATGCAATCTGGAAGC-----CAATCAT 1563
 Oy 1519 CCCTTGCTCGGGCTGTCTTACCTCCCTTGTGTGGCCACAGTTACCATTTTGATGAT 1578
 Db 1564 GTTCTTACACTGTTGCTGCTCCGATCTCCCTCCACTGACAGTAACTTTTGTATGAT 1623
 Oy 1579 GACCATGAGAGCATCTTCACTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1638
 Db 1624 GACCAAGAGAGCATTTTACTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1683
 Oy 1639 GTTATGAGAGTCAAGGTTCTGCGACATCAGTGTCCCGGGTACAGTCACTGCTCCCTTT 1698
 Db 1684 ATCATGAGAGTGAAGATATGAGAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1743
 Oy 1699 AGGACAGTGAAG 1758
 Db 1744 AAACCATCAG 1803
 Oy 1759 TTGGAATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1788
 Db 1804 CTCGAATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833

RESULT 14

ABSI2734 ID ABSI2734 standard; DNA; 1836 BP.

XX ABSI2734;

XX 19-AUG-2002 (first entry)

DE Human genome-derived single exon probe ORF from lung SEQ ID No 12725.

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KM chronic obstructive pulmonary disease; interstitial lung disease;
 KM familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KM tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KM Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KM pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KM pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KM primary ciliary dyskinesia; pulmonary hypertension;
 KM hyaline membrane disease; open reading frame; ORF.

OS Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US00665.

XX 04-FEB-2000; 2000US-180312P.

XX 26-MAY-2000; 2000US-207456P.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0633366.

XX 21-SEP-2000; 2000US-234687P.

XX 27-SEP-2000; 2000US-236359P.

XX 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 PS
 XX Claim 4: SEQ ID No 12725; 634bp; English.

CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the labeled nucleic acids bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a single exon
 CC probe open reading frame of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;

Query Match 28.5%; Score 787.2; DB 24; Length 1836;

Best Local Similarity 68.3%; Pred. No. 3; 9e-216;

Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

Oy 109 GAGTCCCAAGCAGGAGGAGCAAGCAATGAGTCTGTTAGAGTCAAGGAGCAAGAGAG 168
 Db 133 GAATGAG 192
 Oy 169 GGTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 228
 Db 193 GGGGTGATTTTGGCCATTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
 Oy 229 GTCATGTCATTTTGGCCGATATATGATGATGATGATGATGATGATGATGATGATGATGAT 288
 Db 253 GCTACGTGATTTTGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
 Oy 289 CGCTTATGATCTATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 348
 Db 313 CGGTGATGATCTCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
 Oy 349 CCCAATGAG 408

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Db      373 CCCAATGAGAGAGACACCAACAACTGTGAGATCTGGAAATGAAAGTTTCAACCTG 432
Qy      409 ACCCTTATGGCCCTGGGCTTCCTGCTCTGAGATACCTCTCTTTAATGAGCTGT 468
Db      433 ACCCTGATGGCCCTGGGATCTTCTGCTCTGAGATTTCTCTTTAGTAATGAAAGTGT 492
Qy      469 GGTGATGGGTTCAATGCTGTGATCTGGAGACCTTCTACATTTGTAAGGAGTGACGCTTC 528
Db      493 GGCATTAACCTCACTGAGGAGACCTCGGTCCTAGCACATCGTGGGAAGTGTGACATTC 552
Qy      529 AACATGTTCAATCATATGGCATGTGTGTCTAGCTGATCCAGACGAGAGACTGCGAAG 588
Db      553 AATATGTTCAATCATATTAATGACACTGTGTATGTGTGTGCTGACGAGAGAACAAAGAG 612
Qy      589 ATCAAGATCATACAGATCTTCTTCATCACGCTCTTGAGATATCTTGGCTACATGTG 648
Db      613 ATTAAGCATTTGGCTGTCTTCTTGTGACAGACGCTGAGACATCTTGGCTACACCTGG 672
Qy      649 CTCTAATATGATTCGAGATCTTCTCCCTGGTGTGCTCAGATTTGGGAAGCCCTCTC 708
Db      673 CTTCATATTAATTTTGTGTGATATCTCTGCTGTGTGAGAGTCTGGGAAGTTGCTT 732
Qy      709 ACTGCTCTTCTTCTTCCAGTGTGTGTCTCTGCTGTGGCTGGGAGAGATAAACGCTGCTC 768
Db      733 ACTTCTCTTCTTCTTCCATCTCTGTGTGTGTGCTGGGAGAGATAGGAGACTCTGT 792
Qy      769 TTCTACAAATACATGACACAAAATACCGCAGACAAACACCGAATATATCATAGAG 828
Db      793 TTTTACAAAGATGTCTACAAAGAGATATCGAGCTGCGAAGCAGAGGGGATATTAATGAA 852
Qy      829 ACAGAGGGTGACACCC-----TAAGGCAATTGAGATGATGGGAAATGATGAT 879
Db      853 CATGAAAGAGACAGCCACTTCTTAAGACTGAATTAATGAATGAGCGGAAAGTGTGCT 912
Qy      880 TCCCATTTTCTAGTGGGAACCTGTGCTCCCTGGAAGGAAAG----- 921
Db      913 TCTCATGTGAAATTTCTTAGATGTGTGTGCTGTGAGGTGATGAGAGGGACCA 972
Qy      922 GAAGTGTATGATCCCGCAGAGATGATCCGATTTCTCAAGATCTGAACAAAACAC 981
Db      973 GATGATGAAGAGCTAGCGCGAAGATGCTAGATTTCTGAAGAACATTAACAGAACAT 1032
Qy      982 CCAGAGAGAGACTTATGATCAAGCTGTGTGAGATGCGCAATTAATGCTTTTCCACCAA 1041
Db      1033 CCAGATTAAGAAATAGACAAATTAATAGAAATTAACCTAAGCTTAAGCTACAGAG 1092
Qy      1042 CAGAAGAGCCGCGCTCTACCCATATCCAAAGCCATGATGATGATGATGATGATGATGAT 1101
Db      1093 CAAAAGAGTGAAGCATTTTATCGCATTCAGCTACCTGCTCATGACTGAGAGCTGGCAAC 1152
Qy      1102 ATCTGAGAGAAACATGCGAGAGAACCAAGAGCCCTCCACATGAGAGAGTGTGCAC 1161
Db      1153 ATTTTAAAGAGCATGACGCTGACCAAGCAAGAGAGAGCTGTGACAGATGACAGAGTCAAC 1212
Qy      1162 ACCGATAGCCCTG--AGACTTATTTCCAGAGCTCTTGTGACCATGTTCTTACAG 1218
Db      1213 ACTGAATGACTGAATAATGACCCCTGTTAGTAAGATCTTCTTGAACAAGGACATATACAG 1272
Qy      1219 TGCTGAGAACTGTGGGCTGTACTCTGTACAGTGTGTGAGAAAGGGGAGACATGTCA 1278
Db      1273 TGCTGAGAACTGTGTACTGTGTGCTTACCTTACATTTATCCGACAGAGTGTGATTTACT 1332
Qy      1279 AGACCATGATATGATGACAAACAAAGAGAGATGTTCTGCCATGAGAGGCTGACATAT 1338
Db      1333 AACCTGTGTTGTTGCTTCAACAGAGAGATGGCACAGAAATGCTGGTCTGATTAAT 1392
Qy      1339 GAGTTTCAAGAGGAGCGTGTGTCTGAGACGAGAGAGACCCAGAGAGATTTCTCCGTG 1398
Db      1393 GAATTTTCTGAGAGAACTGTGTGTTTAAGCCTGTGATACCCGAAGAAATAGAGTGT 1452
Qy      1399 GGCATTAATGATGACGACATTTTGGAGAGAGTGAACACTTCTTGTGAAGGTTGAGCAAT 1458

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Db      1453 GGTATCATATGATGATATCTTTGAGAGAGATGAATAATTTCTTGTGATCTCAGCAAT 1512
Qy      1459 GTCCGATATAGAGAGAGACAGCAGAGAGAGGATGCTCCAGCAATATTCACAGTCTT 1518
Db      1513 GTCAAGATATCTTCTGAAAGCTGTGAAAGATGGATGCACTAGTGAAGC-----CAATCAT 1563
Qy      1519 CCCTTGCTGGGGCTGTCTAGACCTCCCTTGTGTGAGCCACAGTATACATCTTGATGAT 1578
Db      1564 GTTCTTCACTATGCTTCCCTGAGATCTCCCTCCACTGCACTGTAACTAATTTTGAATGAT 1623
Qy      1579 GAACTGACGAGCATCTCACTTGTGAATGTGATCTATTCATGATGACAGATATGAT 1638
Db      1624 GACCCAGCAGCATTTTACTTGTGAGAACCTGTGACTCATGTGAGTGAAGATTTGGC 1683
Qy      1639 GTTATGAGAGGTCAAGTTTCCGAGCATCAAGTGTCCCGGATACATCATCTCCCTTT 1698
Db      1684 ATCATGAGAGGTGAAGATTTAGAACATCTGAGACTGTGAGAAATGTTATGTTCCATAT 1743
Qy      1699 AGGACATGAGAGGAGACCCAGAGGCTGGGCTGAGACATTTGAAGACATATGAGGAG 1758
Db      1744 AAACCATCGAAGGAGACTGCCAGAGGTGAGAGGAGATTTTGAAGACACTTGTGAGAG 1803
Qy      1759 TTGGAATTCAGATGATGAATAACCTGAAA 1788
Db      1804 CTGCAATTCAGAAATGAAATTTGTGAA 1833

RESULT 15
ABL09809
ID ABL09809 standard; cDNA; 4546 bp.
XX
AC ABL09809;
XX
DE 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23909.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN W0200171042-A2.
XX
PD 27-SEP-2001.
XX
PE 23-MAR-2001; 2001MO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB65706.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 23909; 21bp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB5737-ABB72072).
CC The sequence data for this patent did not form part of the printed

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Db 2585 TACGTAGCCACTTCGTCCCTCTTTGGAGAGTTCTTTGGCATTTGTGCCCCACT 2644
QY 2230 GAGTACGACACGGGCTGGGCTGTGGCTTCATTCCTCATTCATTCATTCATTCATTC 2289
Db 2645 GACATTTGGCGGGCTATGTACCTTTGTGTATCCATATTCGTGATTTGGCGTCATCCT 2704
QY 2290 GCCATCATTTGGGACCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2349
Db 2705 GCCATCATTCGGAGATGGCGCTCCTATTTGGGCTGGCGCTTCACATCAAGAGACTGGTA 2764
QY 2350 ACAGCTGTCTTTCTGGCATTTGGCATTCGTCTGTCCATATTCATTCATTCATTCAT 2409
Db 2765 ACAGGCTATTCCTGTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 2824
QY 2410 GCTGCCCTTCAGATGATATGACAGACCTTCATTTGGCAACGTCAGGGGAGCAAGCC 2469
Db 2825 GCCGCCACGATGACAGAGGCTGGGATATTCATTCATTCGCAATGTCACGGGAGCAATGCG 2884
QY 2470 GTCATATCTTCTCTGGGCTATCGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 2529
Db 2885 GTCAGGCTGTCTCGGGCTATCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 2944
QY 2530 CAGGAGACGAGATTCCAGCTGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 2589
Db 2945 CATGGGATGACCTTCACAGCTGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 3004
QY 2590 ATCTTTGATTTGCTGCTATCGAGGCTGTCTTTGACCGAAGGGGCT--CGACCTGGGA 2646
Db 3005 GCGAGGCTCTGATTTGCTATATGCTATCATATGTTCCGGGCTGGGCTGGGCTGGGCT 3064
QY 2647 GGGGAGCTTGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 2706
Db 3065 GCGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 3124
QY 2707 TGGCTCTCTACATCTCTTTGGCACACTAGAGGCTATTTGCTACATCAAGG 2758
Db 3125 TGGGTGTTCTACGTTATATGCTATGCTAGAGGCTTACGAGCTTACGAGCTATCCGGG 3176
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